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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:00:26 ; Search time 194 Seconds
(without alignments)
1256.986 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIVAILISINACIGLMNAS.....IMPCPPGTWQEKLTICGE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3107	100.0	555	AAV52523	Aay52523 House dus
2	3107	100.0	555	AAU96327	Aau96327 Der HMW-m
3	3107	100.0	555	AAU96328	Aau96328 Der HMW-m
4	3014	97.0	536	AAU96329	Aay52525 House dus
5	3014	97.0	536	AAU96329	Aau96329 Der HMW-m
6	2542	81.8	509	AAV52533	Aay52533 D. pteron
7	2542	81.8	509	AAU96337	Aau96337 Der HMW-m
8	2542	81.8	509	AAU96338	Aau96338 Der HMW-m
9	2475	79.7	490	AAV52535	Aay52535 D. pteron
10	2475	79.7	490	AAU96339	Aau96339 Der HMW-m
11	1008.5	32.5	525	ABP72636	Abp72636 Anopheles
12	854.5	27.5	4498	ABB58595	Abb58595 Drosophil
13	838.5	27.0	554	AAW01824	Aaw01824 Manduca s
14	838.5	27.0	554	AAW01824	Aaw01824 Manduca s
15	838.5	27.0	554	ABP72619	Abp72619 Manduca s
16	837.5	27.0	467	ABP72634	Abp72634 Prawn chi
17	837.5	27.0	565	ABP72625	Abp72625 Bombyx mo
18	837.5	27.0	595	ABP71737	Abp71737 Drosophil
19	832	26.8	460	ABB64366	Abb64366 Drosophil
20	815.5	26.2	583	AAE28197	Aae28197 Flea chit
21	812.5	26.2	635	AAE28203	Aae28203 Flea chit
22	811.5	26.1	559	AAE28199	Aae28199 Flea Pcfc
23	810	26.1	574	ABP72635	Abp72635 Aedes aeg
24	802	25.8	483	ABP72633	Abp72633 Chelonus

25	787	25.3	553	6	ABP72626	Abp72626 Hyphantri
26	738	23.8	444	8	ADQ59635	Adq59635 Chitotrio
27	738	23.8	466	2	AAW08584	Aaw08584 Human 50
28	738	23.8	466	2	AAW40259	Aaw40259 Human chi
29	738	23.8	466	2	AAV42425	Aay42425 MO-218 cl
30	738	23.8	466	4	AAE00432	Aae00432 Human chi
31	738	23.8	466	5	AAE25903	Aae25903 Human chi
32	738	23.8	466	5	ABB76291	Abb76291 Human chi
33	738	23.8	466	7	ABW00767	Abw00767 Human chi
34	738	23.8	466	8	ADQ18533	Adq18533 Human sof
35	738	23.8	466	8	ADQ59634	Adq59634 Chitotrio
36	738	23.8	466	9	ADZ80444	Adz80444 Mature ch
37	737.5	23.7	520	6	ABU09914	Abu09914 Partial m
38	736.5	23.7	473	7	ABR55543	AbR55543 Amino aci
39	736.5	23.7	473	8	ADT92466	Adt92466 Murine ac
40	735.5	23.7	459	7	ADC24231	Adc24231 Human NOV
41	734.5	23.6	473	7	ADC51464	Adc51464 Chitotria
42	732.5	23.6	387	2	AAW08585	Aaw08585 Human 39
43	732	23.6	447	7	ADC24237	Adc24237 Human NOV
44	732	23.6	466	2	AAW40260	Aaw40260 Human chi
45	732	23.6	466	2	AAV42426	Aay42426 MO-13B cl

ALIGNMENTS

RESULT 1
AAV52523
ID AAY52523 standard; protein; 555 AA.
XX
AC AAY52523;
XX
DT 22-FEB-2000 (first entry)
XX
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides farinae.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "Signal peptide"
FT /note= "Mature PDerf98-555"
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
(HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2000-052700/04.
XX
N-ESDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX
Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivity to mite allergens.
XX
Claim 3; Page 111-113; 154pp; English.
XX
This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,

CC comprising 555 amino acids, and is a component of the Dermatophagoides
CC farinae high molecular weight mite allergen protein (HWM-map)
CC composition. The HWM-map composition was isolated from a D. farinae
CC homogenate by gel filtration, with each fraction being analysed for the
CC presence of proteins that bound to IgE present in mite-allergic dog
CC antiserum. Mite allergenic proteins and peptides, and nucleic acids
CC encoding them, may be used in therapeutic compositions to modify an
CC animal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The
CC proteins and peptides can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
DB 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60

QY 61 CTHLMYGAKEIDYKYTIQVDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
DB 61 CTHLMYGAKEIDYKYTIQVDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120

QY 121 EGSEKYSDMAANPTVYRQFIQSVLDFLQEKYKFDGLDWEYPSGLGNPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANPTVYRQFIQSVLDFLQEKYKFDGLDWEYPSGLGNPKIDKQNYLALV 180

QY 181 RELKDAFEPHGYLLTAAVSPGDKIDRAYDIKELNKLFDWMNVMTYDHYGGWENFYGHNA 240
DB 181 RELKDAFEPHGYLLTAAVSPGDKIDRAYDIKELNKLFDWMNVMTYDHYGGWENFYGHNA 240

QY 241 PLYKRPDETDLHTYFNVNYTHYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDETDLHTYFNVNYTHYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLGDPGA 300

QY 301 KGMSPPGFISGEEGVLSEIQLCFQKEEWHIQYDEYNNAPYGYNDKIWVGVDLILASISC 360
DB 301 KGMSPPGFISGEEGVLSEIQLCFQKEEWHIQYDEYNNAPYGYNDKIWVGVDLILASISC 360

QY 361 KLAFLKELGVSGVMVWSLENDPFKHCQPKNPLLNKVNMMINGDEKNSPECILGPSTTTP 420
DB 361 KLAFLKELGVSGVMVWSLENDPFKHCQPKNPLLNKVNMMINGDEKNSPECILGPSTTTP 420

QY 421 TPPTTPT 480
DB 421 TPPTTPT 480

QY 481 TPSPPTTHTSTPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVEFVNGGWWHIMPCP 540
DB 481 TPSPPTTHTSTPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVEFVNGGWWHIMPCP 540

QY 541 PGTIWCQEKLTICGE 555
DB 541 PGTIWCQEKLTICGE 555

RESULT 2
AAU96327
ID AAU96327 standard; protein; 555 AA.

XX AAU96327;

XX 15-JUL-2002 (first entry)

XX Der HWM-map polypeptide #14.

XX Der HWM-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX WO200222807-A2.
XX 21-MAR-2002.
XX 14-SEP-2001; 2001WO-US028730.
XX 14-SEP-2000; 2000US-00662293.
XX (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
XX WPI; 2002-351888/38.
DR N-PSDB; ABK69571.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HWM-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 114-116; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic
CC acid. The Der HWM-map protein is useful for eliciting an immune response
CC against Der HWM-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a
CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HWM-map polypeptides of the invention
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
DB 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60

QY 61 CTHLMYGAKEIDYKYTIQVDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
DB 61 CTHLMYGAKEIDYKYTIQVDPYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120

QY 121 EGSEKYSDMAANPTVYRQFIQSVLDFLQEKYKFDGLDWEYPSGLGNPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANPTVYRQFIQSVLDFLQEKYKFDGLDWEYPSGLGNPKIDKQNYLALV 180

QY 181 RELKDAFEPHGYLLTAAVSPGDKIDRAYDIKELNKLFDWMNVMTYDHYGGWENFYGHNA 240
DB 181 RELKDAFEPHGYLLTAAVSPGDKIDRAYDIKELNKLFDWMNVMTYDHYGGWENFYGHNA 240

QY 241 PLYKRPDETDLHTYFNVNYTHYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDETDLHTYFNVNYTHYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLGDPGA 300

QY 301 KGMSPPGFISGEEGVLSEIQLCFQKEEWHIQYDEYNNAPYGYNDKIWVGVDLILASISC 360
DB 301 KGMSPPGFISGEEGVLSEIQLCFQKEEWHIQYDEYNNAPYGYNDKIWVGVDLILASISC 360

XX WPI; 2000-052700/04.
DR N-PSDB; AAZ38579, AAZ38580.
XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivity to mite allergens.
XX
XX
PS Claim 3; Page 125-127; 154pp; English.
XX This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) PDerf98-536, the mature form of PDerf98-555 (AAV52523). PDerf98-536
CC has a molecular weight of 98 kD, comprising 536 amino acids, and is a
CC component of the Dermatophagoides farinae high molecular weight mite
CC allergen protein (HWM-map) composition. The HWM-map composition was
CC isolated from a D. farinae homogenate by gel filtration, with each
CC fraction being analysed for the presence of proteins that bound to IgE
CC present in mite-allergic dog antisera. Mite allergenic proteins and
CC peptides, and nucleic acids encoding them, may be used in therapeutic
CC compositions to modify an animal's hypersensitivity reaction to mite
CC allergens. Animals that may be treated include mammals and birds,
CC especially felines, canines, equines, humans, other pets, and work or
CC domestic animals. The proteins or fragments may also be used to diagnose
CC allergies via a skin test. The proteins and peptides can also be used to
CC raise antibodies, which have a variety of potential uses. For example,
CC they can be used as vaccines to passively immunise animals against dust
CC mite hypersensitivity, as positive controls in test kits and as tools to
XX recover desired dust mite allergens from a mixture of proteins
XX
XX Sequence 536 AA;

Query Match 97.0%; Score 3014; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.3e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SIKRDNDYKNPMRIVCVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADIKYTIQ 79
DB 1 SIKRDNDYKNPMRIVCVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADIKYTIQ 60
QY 80 VFDPYQDDNHNHNSWEGYERFNNRLKNPELTTMISLGGWYEGSEKYSDMAANPYRQOF 139
DB 61 VFDPYQDDNHNHNSWEGYERFNNRLKNPELTTMISLGGWYEGSEKYSDMAANPYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDLDWEYPGSRNLGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVS 199
DB 121 IQSVLDFLOEYKFDGLDLDWEYPGSRNLGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 259
DB 181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHMYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGLSVI 319
DB 241 YTHMYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGLSVI 300
QY 320 ELCQLFQKEWHIQDEYNNAPYGNDKIWWGYDDLASISCKLAFKELGVSGVNVWSLE 379
DB 301 ELCQLFQKEWHIQDEYNNAPYGNDKIWWGYDDLASISCKLAFKELGVSGVNVWSLE 360
QY 380 NDDFKGHGCPKNPLKNVHNMINGDKNSFCILGPSSTTTPTPTPTPTPTPTPTPTPTPTPT 439
DB 361 NDDFKGHGCPKNPLKNVHNMINGDKNSFCILGPSSTTTPTPTPTPTPTPTPTPTPTPTPT 420
QY 440 TPT 499
DB 421 TPT 480
QY 500 VDGHILKCYKEGDIHPHTNIHKLVCEFVNGWVHIMPCCPGTTCWCEKLTICGE 555
DB 481 VDGHILKCYKEGDIHPHTNIHKLVCEFVNGWVHIMPCCPGTTCWCEKLTICGE 536

RESULT 5
AAU96329

ID AAU96329 standard; protein; 536 AA.
XX
AC AAU96329;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HWM-map polypeptide #16.
XX
KW Der HWM-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
XX immunocomplex formation.
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX (HESK-) HESKA CORP.
XX
PI McCall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69575.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HWM-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 125-127; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic
CC acid. The Der HWM-map protein is useful for eliciting an immune response
CC against Der HWM-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig) E or Der HWM-map protein activity associated with a
CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HWM-map polypeptides of the invention
XX
SQ Sequence 536 AA;

Query Match 97.0%; Score 3014; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.3e-210;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SIKRDNDYKNPMRIVCVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADIKYTIQ 79
DB 1 SIKRDNDYKNPMRIVCVGTWSVYHKVDPTIEDIDPFKCTHLMYGFADIKYTIQ 60
QY 80 VFDPYQDDNHNHNSWEGYERFNNRLKNPELTTMISLGGWYEGSEKYSDMAANPYRQOF 139
DB 61 VFDPYQDDNHNHNSWEGYERFNNRLKNPELTTMISLGGWYEGSEKYSDMAANPYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDLDWEYPGSRNLGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVS 199
DB 121 IQSVLDFLOEYKFDGLDLDWEYPGSRNLGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVS 180
QY 200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 259
DB 181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYGWENFYGHNAPLYKRPDETDELHTYFNVN 240
QY 260 YTHMYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPKAGMSPPGFISGEEGLSVI 319

241	YTHYYLNNGATRD	KL	VMGVFPYGRAMS	IEBRS	SKL	IGDPAK	SGMSPPGF	ISGSEGVLS	300
320	ELCQLQFQKEB	HIQYDE	YNNAPY	GYNDKI	WYGYDD	LASIS	CKLAFL	KELG	379
301	ELCQLFQKEB	HIQYDE	YNNAPY	GYNDKI	WYGYDD	LASIS	CKLAFL	KELG	360
380	NDDFKGHC	CPKPNLLK	VHNNIM	GBKNS	FCILGP	STTTPT	TTTTPT	TTTTPT	439
361	NDDFKGHC	CPKPNLLK	VHNNIM	GBKNS	FCILGP	STTTPT	TTTTPT	TTTTPT	420
440	TPTTTTSP	TTTTSP	TTTTSP	TTTTSP	TTTTPT	TPAT	STSTSP	TTTTST	499
421	TPTTTTSP	TTTTSP	TTTTSP	TTTTSP	TTTTPT	TPAT	STSTSP	TTTTST	480
500	VDGHLIKCY	KEGDI	PHPTNI	KHLY	CEFPV	GGWV	WHMPC	PPGT	555
481	VDGHLIKCY	KEGDI	PHPTNI	KHLY	CEFPV	GGWV	WHMPC	PPGT	536

RESULT 6

RESULT 0
AAY52533
ID AAY52533 standard: protein: 509 AA.

AC AAY52533;

XX DT 06-AUG-2003 (revised)

DT	06-AUG-2003	(revised)
DT	22-FEB-2009	(first entry)

DE D. pteronyssius 98 kD mite allergen protein (map) pDerp98-509.

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite, IgE; immunoglobulin E; allergen: map8;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides pteronyssinus.

XX	Key	Location/Qualifiers
FH		

FT	Peptide	1. .19	1. .19
FT	Peptide	1. .19	1. .19

FT	/note= "Signal peptide"
100-109	
110-119	
120-129	
130-139	
140-149	
150-159	
160-169	
170-179	
180-189	
190-199	
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240-249	
250-259	
260-269	
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560-569	
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580-589	
590-599	
600-609	
610-619	
620-629	
630-639	
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900-909	
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930-939	
940-949	
950-959	
960-969	
970-979	
980-989	
990-999	

FT	Protein	20.	.50
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4	4	4	4
5	5	5	5
6	6	6	6
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8	8	8	8
9	9	9	9
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11	11	11	11
12	12	12	12
13	13	13	13
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74	74	74	74
75	75	75	75
76	76	76	76
77	77	77	77
78	78	78	78
79	79	79	79
80	80	80	80
81	81	81	81
82	82	82	82
83	83	83	83
84	84	84	84
85	85	85	85
86	86	86	86
87	87	87	87
88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

FT /note= "Mature pDerp98-509"

XX
PN WO9954349-A2.

28-OCT-1999.

XX
PF 16-APR-1999: 99WO-US008524.XX
PR 17-APR-1998: 98US-00062013.

17-AFK-1998; 98US-0000295P;
13-MAY-1998: 98US-0085295P;

PR 02-SEP-1998; 98US-0098909P;

PA (HESK-) HESKA CORP.

PI Mccall CA, Hunter SW, Weber ER;

DR WPI; 2000-052700/04.

DR N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.

PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivity to mite allergens.

PS Claim 3: Page 134-136; 154pp; English.

AA CC This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) Pderp98-509 has a molecular weight of 98 kD, CC comprising 509 amino acids, and has a high degree of homology with the D. CC farinae 98 kD allergen, map9 (AAV52523). Nucleic acid molecules encoding CC Pderp98-509 were isolated from a D. pteronyssius cDNA library by CC hybridisation with a probe encoding the D. farinae high molecular weight CC allergen (HMW-map) composition. Mite allergenic proteins and peptides, and CC

OS Dermatophagoides farinae.
XX WO200222807-A2.
PN 21-MAR-2002.
XX 14-SEP-2001; 2001WO-US028730.
XX 14-SEP-2000; 2000US-00662293.
PR (HESK-) HESKA CORP.
XX
XX Mccall CA, Hunter SW, Weber ER;
XX WPI; 2002-351888/38.
DR N-PSDB; ABK69581.
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
XX Claim 12; Page 134-136; 161pp; English.
XX
XX The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (IgE or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 509 AA;
Query Match 81.8%; Score 2542; DB 5; Length 509;
Best Local Similarity 81.7%; Pred. No. 2.6e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLNMASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
DB 1 MKTTFALFCIWACIGLNMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
QY 61 CTHLMYGFADIDYKYITQVDFPDYODDHNHNSKEKGYERFNNLRKLNPELTMTMISLGGWY 120
DB 61 CTHLMYGFADIDYKYITQVDFPDYODDHNHNSKEKGYERFNNLRKLNPELTMTMISLGGWY 120
QY 121 EGSEKYSDMAANTYRQPFQVQVSLDFLQBYKFDGLDWEYSGSLGNPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANTYRQPFQVQVSLDFLQBYKFDGLDWEYSGSLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAASVPGKDKIDRAYIDIKELNKLFDMMVMVYDHYHGWENPYGNA 240
DB 181 RELKEAFEPGYLLTAASVPGKDKIDVAYELKELNQLFDMVMVMVYDHYHGWENPYGNA 240
QY 241 PLYKRPDETHLYTFVNNYTHYYLNNCATDKLVMGVPFGYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDETHLYTFVNNYTHYYLNNCATDKLVMGVPFGYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPPGFTSGEGVLSYELCQLFOKEWHIYQDEYNNAPYGYNDKIWVGVDLILASISC 360
DB 301 KGMSPPGFTSGEGVLSYELCQLFOKEWHIYQDEYNNAPYGYNDKIWVGVDLILASISC 360
QY 361 KLAFLKELGVSGVMWSLENDPDKGHCGRPKNPLNKNVHNMINGDEKNSFECILGSPSTTP 420
DB 361 KLAFLKELGVSGVMWSLENDPDKGHCGRPKNPLNKNVHNMINGDEKNSFECILGSPSTTP 420
QY 421 TPTTPT 480

DB 421 TPTTPT 434
QY 481 TPSETTTTSETPKYTYTYVDGHLIKCYKEGDI PHTPHNIHKYLYCFV---NGGWWVHIM 537
DB 435 ---PTTDTSTSETPKYTYTYVDGHLIKCYKQGLPHTPDVHKYLYCEVIATNGGWWVHIM 491
QY 538 PCPFGTTWCQEKLTICIG 555
DB 492 DCPKGTWRHATLKNKICIG 509
RESULT 8
AAU96338
ID AAU96338 standard; protein; 509 AA.
XX
AC AAU96338;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #25.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
OS Dermatophagoides farinae.
XX WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
XX WPI; 2002-351888/38.
DR N-PSDB; ABK69583.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 139-141; 161pp; English.
XX
XX The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (IgE or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 509 AA;
Query Match 81.8%; Score 2542; DB 5; Length 509;
Best Local Similarity 81.7%; Pred. No. 2.6e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLNMASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
DB 1 MKTTFALFCIWACIGLNMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPTIEDIDPFK 60
QY 61 CTHLMYGFADIDYKYITQVDFPDYODDHNHNSKEKGYERFNNLRKLNPELTMTMISLGGWY 120
DB 61 CTHLMYGFADIDYKYITQVDFPDYODDHNHNSKEKGYERFNNLRKLNPELTMTMISLGGWY 120
QY 121 EGSEKYSDMAANTYRQPFQVQVSLDFLQBYKFDGLDWEYSGSLGNPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANTYRQPFQVQVSLDFLQBYKFDGLDWEYSGSLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAASVPGKDKIDRAYIDIKELNKLFDMMVMVYDHYHGWENPYGNA 240
DB 181 RELKEAFEPGYLLTAASVPGKDKIDVAYELKELNQLFDMVMVMVYDHYHGWENPYGNA 240
QY 241 PLYKRPDETHLYTFVNNYTHYYLNNCATDKLVMGVPFGYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDETHLYTFVNNYTHYYLNNCATDKLVMGVPFGYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPPGFTSGEGVLSYELCQLFOKEWHIYQDEYNNAPYGYNDKIWVGVDLILASISC 360
DB 301 KGMSPPGFTSGEGVLSYELCQLFOKEWHIYQDEYNNAPYGYNDKIWVGVDLILASISC 360
QY 361 KLAFLKELGVSGVMWSLENDPDKGHCGRPKNPLNKNVHNMINGDEKNSFECILGSPSTTP 420
DB 361 KLAFLKELGVSGVMWSLENDPDKGHCGRPKNPLNKNVHNMINGDEKNSFECILGSPSTTP 420
QY 421 TPTTPT 480

RESULT 10	
AAU96339	
ID	AAU96339 standard; protein; 490 AA.
XX AC	
XX AC	AAU96339;
DT	15-JUL-2002 (first entry)
XX XX	
DE	Der HMW-map polypeptide #26.
XX XX	
KW KW	Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW KW	mite allergenic protein; immunoglobulin E; hypersensitivity;
KW KW	immunocomplex formation.
XX OS	
XX OS	Dermatophagoidees farinae.
PN PN	
XX PN	WO20022807-A2.
XX PD	21-MAR-2002.
XX PP	14-SEP-2001; 2001WO-US028730.
XX PR	14-SEP-2000; 2000US-00662293.
XX PA	(HESK-) HESKA CORP.
XX PI	Mccall CA, Hunter SW, Weber ER;
XX DR	WPI; 2002-351888/38.
DR N-PSDB;	ABK69585.
XX XX	
PT PT	New mite allergenic protein isolated from Dermatophagoides, designated
XX XX	Der HMW-map protein, useful as a vaccine for treating mite allergy.
PS	Claim 12; Page 144-146; 161pp; English.
XX CC	The invention relates to an isolated mite allergenic protein of
CC CC	Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC CC	acid. The Der HMW-map protein is useful for eliciting an immune response
CC CC	against Der HMW-map protein. The protein or a reagent comprising a non-
CC CC	proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC CC	cat) susceptible to or having an allergic response to a mite. A
CC CC	therapeutic composition is useful for desensitizing a host animal to an
CC CC	allergic response to a mite. The DNA and protein can be used in the
CC CC	detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC CC	of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC CC	disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC CC	binding of proteins to IgE, to prevent immunocomplex formation, thus
CC CC	reducing hypersensitivity responses to mite allergens, and as vaccines
CC CC	against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX CC	represent Der HMW-map polypeptides of the invention
SQ	Sequence 490 AA;
Query Match	79.7%; Score 2475; DB 5; Length 490;
Best Local Similarity	82.5%; Pred. No. 1.9e-171;
Matches 443; Conservative	21; Mismatches 21; Indels 52; Gaps 2;
QY	22 KRDNHYSKNPMRIVCVGVTSVYHKVDPTTIEDIDPFKCTHLMVGFAKIDYKYTIQVF 81
Db	3 KRDNHYSKNPMRIVCVGVTSVYHKVDPTTIEDIDPFKCTHLMVGFAKIDYKYTIQVF 62
QY	82 DPVOODNHNHNSWEKRGYVERFNNLRKNPELTTMISLGWYEGSEKYSDMAANTYRQQFIQ 141
Db	63 DPODDNHNHNSWEKHGVERFNNLRKNPELTTMISLGWYEGSEKYSDMAANTYRQQFVQ 122
QY	142 SVLDLFQEKYKFDGLDWEYPGSRGNPKDKQNLYALVRELKDAFEHPHGYYLLTAASVSG 201
Db	123 SVLDFFQEKYKFDGLDWEYTPGSRGNPKDKQNLYLVRELKEAPEPPFGYLLTAASVSG 182
QY	202 KKIDRAYDIKELNFLDMNVNMTYDYHGWNFYGHNAPLYKRPDETDELTYFNVTY 261
Db	183 KKDIDVAYEKELNOLFDNMVNMTYDYHGWNFVGHNAPLYKRPDETDELTYFNVTY 242

CC The present sequence is that of the mosquito *Anopheles gambiae* chitinase.
CC This protein is used in claimed fusion proteins of the invention. Such
CC fusion proteins comprise a translocating moiety and a toxic moiety, where
CC the translocating moiety is a plant protein (e.g. a lectin) capable of
CC acting as a carrier to translocate the toxic moiety across the gut wall
CC of a plant pathogen, and the toxic moiety is an insect-derived peptide or
CC protein capable of causing deleterious effects on growth, development,
CC reproduction or mortality in pest insects. Suitable insect peptides and
CC proteins include allatostatin, chitinase, diuretic hormone and their
CC metabolites and analogues. Polynucleotides encoding the fusion protein,
CC vectors, host cells and transgenic plants that are resistant to disease
CC are also provided. The fusion protein is target-specific, and resists
CC degradation in the insect gut

XX SQ Sequence 525 AA;

Query Match 32.5%; Score 1008.5; DB 6; Length 525;
Best Local Similarity 38.4%; Pred. No. 1.1e-64;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

QY 8 LSTMACIGLNASIKED-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM 65
DB 5 VGVLLVAVAAAFABEPHKAASAECKVVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLM 64
QY 66 YGPAKIDYKTIQVDPYODDNHNSWEKRGYERFNNLRKLNPELTMTISLGGWEGSEK 125
DB 65 YGPFGLNE-DATVRIIDPVLDEEN-WGRGHKIKRFVGLKNVGFGLKTLAAGWEGSRK 122
QY 126 YSDMAANPTVROQFIQSVLDFLQYKFDGLDLDWEYPSGRNLGNPKIDKQNYLALVRELK 185
DB 123 FSAMAASGELRKRFISDCVAFQCRHGFHDGLDWEYPAQRDGNFLIDRDHNAQLVEEMRE 182
QY 186 APEPHGYLTAASVPGKIDRAYDIDKLNKLFDDNNVMTYDYGWENFYGHNAPLYKR 245
DB 183 EFDHYGLLTAASVYEFSGVSYDIPRISKSFHFLNVVMVYDMHGAWDSYCGINAPLYRG 242
QY 246 PDETDLHTVFNVMYTHYVYLNAGATRDKLVMGVPPYGRAWSTEDRSKLKGDPAKGMSP 305
DB 243 SADTDRLGQINVASIHFWLAQCTGRKLVGLGIPLYGRNFTLASAANTQIGAPTGGGT 302
QY 306 PGFISGEGVLSYIELCOLFQKEWHIOYDEYNAPYGYNDKIWVGYYDDLASISCKLAF 365
DB 303 VGRYTREPVGMYNEFCCKLATEAWDLRWSEEQVYAVRNQWVGYYDDLRSVQLKVKYL 362
QY 366 KELGVSGVMVWSLENDDFKHC-GPKNPLLNKVNHNINGDERKNSFECILGPTTPTPT 424
DB 363 LDQGLGAMVWSLETDDFLGVCGGGRYPLMHEIRSLVNGT-----PSTTTPPSV 413
QY 425 TPT 484
DB 414 APTT-----STVAPGTTTTTPTGANPGTQPPT--SDAPNHTTTTBTGNGPTTPPSG 466
QY 485 TTTEHTSETPKYTVYVDGHLIKY--KEGDIPHPTNIHKLVC-----EFVNGGWWVH 535
DB 467 -----DQ---PCAGRGYGVPHPTNCARYICLTADTYEFT----- 500
QY 536 IMPCPGTGW 545
DB 501 ---CPPGTLF 507

RESULT 12

ABBS58595
ID ABBS58595 standard; protein; 4498 AA.

XX AC ABBS58595;

XX DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 2577.

DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.
OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL02698.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from *Drosophila* and for elucidating cell signalling and cell-cell
XX interactions.

XX Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from *Drosophila*. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL6175) and the encoded proteins (ABBS5773-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 4498 AA;

Query Match 27.5%; Score 854.5; DB 4; Length 4498;
Best Local Similarity 33.8%; Pred. No. 2.8e-52;
Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

QY 2 KTIYAILSTMACIGLNASIKRDHNDYSKNPMRIVCYVGTWSVYH---KVDPTYTIEDID 57
DB 33 QTLFLCALAYCI-----NEASSEG-RVVCYVYTNMSVYRPGTAKPNP---QNIN 77
QY 58 PFKCTHLMY---GPAKIDYKTYIQVDPYODDNHNSWEKRGYERFNNLRKLNPELTMT 114
DB 78 PYLCTHLVYAFGGFTKDNQMK---PFDKYQD-----IEQGYAKFTGLKYNKQLKTM 128
QY 115 SLGGHYEGSEKYSDMAANPTVROQFIQSVLDFLQYKFDGLDLDWEYPSGRNLGNPKIDKQ 174
DB 129 AIGGWNEASRRSPPLVASNERRQPFKNILKFLRQNHFDGIDLDWEYPAHREGGSRDRD 188
QY 175 NYLALVRELKDAFEPHG-----YLLTAASVPGKIDRAYDIDKLNKLPDMANVMTYD 227
DB 189 NYAQVQSELRAFEREAETGTRULLLTWAPAGLEYIDKGYDVPKLNKYLDFWVLTVD 248
QY 228 YHGGWENFYGHNAPLYKRPDETDLHTY---FNNVYTHYVYLNAGATRDKLVMGVPPFYGR 284
DB 249 FHSSEPSVNHHAPLYSL--BEDSEYNYDAELNIDYSIKYLYLKAGADRDKLVGLPTYGR 306
QY 285 AWSIEDRSKLKGDPAKGMSPPGFISGEGVLSYIELCOLFQKE--EWH-IQYDEYVYNA 342
DB 307 SYTLINBESSTELGAPAEQPGQDATREKGYLAYVEICQTLKDDPEWTVVQPNANVMGY 366
QY 343 GYNDKIWVGYYDDLASISCKLAFKELGVSGVMVWSLENDDFKHC-GPKNPLLNKVNMI 401
DB 367 AYRNQWVGYYDDALVRKAEYVVAQGLGGINFWAIDNDDFRGTCNGKPYFLIEAA---- 422
QY 402 NGDEKNSPECILGSPSTTTPT 445
DB 423 ----KEAMVEALGLGINEVAKPSGQKPSRSRSDNASNRNLNGKTEAPLSRRPSPATR 478

QY 446 SPTTPTTSPPTPTT-----PSTTPTTPTTPTTPTTPTTPTTTEH 489
DB 479 RPAVSTQAPP--PSTTFKLTAEGSSLYIGRASTTPPTTPTDP----- 522
QY 490 TSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVEFVNG---GWWVHIMPCPPG 542
DB 523 -----GSDFKCEEGFFQHPDRCKKYWC-LDSGSGLGIVAHMFTCPSG 566

RESULT 13

AAW01824
ID AAW01824 standard; protein; 554 AA.
AC AAW01824;
XX
XX
XX 27-MAY-1997 (first entry)
DE Manduca sexta larva epidermal and gut chitinase.
XX Chitinase; insect; transgenic plant; biological control; baculovirus;
KW biocide; insecticide; tobacco hookworm.
XX
OS Manduca sexta.
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT /label= Mat_protein
FT Region 97..111
FT /label= Conserved_region-I
FT Active-site 136..148
FT /note= "proposed active site"
XX
XX WO9708944-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US014440.
XX
XX 06-SEP-1995; 95US-00524051.
XX
XX (UNIV) UNIV KANSAS STATE RES FOUND.
XX
XX Kramer KJ, Muthukrishnan S, Choi HK, Corpuz L, Gopalakrishnan B;
XX
XX WPI: 1997-192586/17.
DR N-PSDB; AAT62557.
XX

Transgenic plant contg. recombinant insect chitinase coding sequence -
useful for controlling plant pests.
PS
PS Claim 4; Page 37-40; 57pp; English.

XX An epidermal and gut chitinase (AAW01824) of Manduca sexta is encoded by
CC cDNA clone 201 (AAT62557), isolated from a day-6 fifth instar whole larva
CC cDNA library. The cDNA can be inserted into a vector for host expression
CC of the chitinase protein, and may be utilised to control a population of
CC insect pests. A recombinant baculovirus vector is provided for this
CC purpose, as well as a transgenic tobacco plant that shows increased
CC resistance to tobacco hornworm. Recombinant chitinase may also be
CC expressed in host cells or larvae for subsequent purification and use as
CC a biocide. The insect chitinase is expected to be more potent as an
CC insect control agent than chitinases from other sources
XX

Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 2.8e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 AILSIWACIGLWNASIKRDNHNSKNPMRIVCVGTWSVYHK-VDPYTIEDIDPPKCTHL 64

DB 3 ATLATLAVLALATAV-----QSDRARIVCYSNWAVRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDKEYKTYIQVDFPYODDNHNSWEKRGYERFNNLRKLNPELTTMISLGGWYEGSE 124
DB 56 IYSGFTGTEGSEVLIIDPELD-----VDKNGFRNFTSLRSSHSPSVKPMVAVGGWAEISS 110
QY 125 KYSDMAANPTTRQOFIQSVLDFLOEYKFDGLDLWEYPGSR-LGNPKLDKQNYLALVREL 183
DB 111 KYSHMVAQKSTRMSFIRSVSFLKKYDFDGLDLWEYFGAADRGGSPSKDKFLYLVQEL 170
QY 184 KDAP--EPHGVLTLTAASPGKIDRAYDIKELANKLPDMVMVMTVDYHGGHENFYGHAP 241
DB 171 RRAFIRVGKWEHTAAVPLANFRLMEGYHVPCLQELDAIHVMSIDLGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNVNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIED----- 290
DB 231 LYKRPD-QWAVEKLVNDGLHWEKGCPSNKLWVGIPFYGRSFTLSAGNNNYGLGTFI 289
QY 291 RSKLKLGPAPKMGSPPGFISGEEGVLVYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
DB 290 NKEAGGGDPAPYTNATGF-----WAYYEICTEVDKDDSGMTKKWDEQGCPCYAYKGTQ 342
QY 349 WVGVDLLASISCKLAFKLKELGVSGVMVWSLENDDFKGHCCKPKNLLNKVHNNINGDEKNS 408
DB 343 WVGVEDPRSVKIKNNWIKQKGYLGAMTWAIIDDFQGLCGEKNPILKILHKMS----- 396
QY 409 FECILGPSTTTPTTPTTPTT-----TTPTTSP-----PTTPTTPTTPTTPTTSP 456
DB 397 -----SYTVPPPHTEHTTTPPEWARPPSTPSPSEGDPIPTTTAKPASTTKTTVKT 449
QY 457 TPTTPTTSPPT-----PTP-TTPTAPTSTSPSTTTEHTSETPKTYTVVDGHLI 505
DB 450 TTTTAKPPQSVIDBEENDINVRPEKPEPQPEVEVP-PTENE-----VDGSEI 497
QY 506 KCYKEGD-IPHPTNIHKYLVEFVNGGWWVHIMPCPGTINCQEKLC 552
DB 498 -CNSDQDYIPDKKCHDKYRWC--VNGE--AMQFSCQRGTVFNVNVLNVC 540

RESULT 14

AAW07183
ID AAW07183 standard; protein; 554 AA.

XX AAW07183;

XX 22-NOV-2000 (first entry)

XX Manduca sexta gut chitinase.

XX

KW Imaginal disc growth factor; IDGF; chitinase related protein; CHRP;
KW tissue growth; wound healing; bone repair; cartilage repair;
KW angiogenesis; meat production; milk production; cancer; gene therapy;
KW gut chitinase.

XX

OS Manduca sexta.

XX US6060590-A.

XX 09-MAY-2000.

XX 31-MAR-1998; 98US-000522778.

XX 31-MAR-1998; 98US-000522778.

XX (REGC) UNIV CALIFORNIA.

XX Bryant PJ, Kawamura K;

XX WPI; 2000-349702/30.

XX New imaginal disc growth factor polypeptide, useful for healing wounds,
XX promoting tissue growth, modulating female reproductive tract functions

PT and treating cell proliferative disorders such as cancer and metastasis.
PS Disclosure; Col 53-58; 40pp; English.
XX
CC The present sequence is the protein sequence for the Manduca sexta gut
CC chitinase. It was used to isolate the Drosophila melanogaster imaginal
CC disc growth factor 4 (IDGF4) coding sequence. IDGF4 is a member of the
CC chitinase related proteins (CHRP) and is involved in the promotion of
CC cell growth, motility and morphogenesis. The gene and protein are
CC expected to have mammalian homologues. They can be used in the treatment
CC of cancer, wound healing, tissue regeneration following arthritis,
CC osteoporosis, other skeletal disorders and burns, for revitalising scar
CC tissue resulting from surgical procedures, irradiation, laceration, toxic
CC chemicals, viral or bacterial infection or burns, to promote tissue
CC growth during tissue engineering, for example tissues for skin graft
CC replacements and bone regrowth, and to modulate the function of the
CC female reproductive tract. In addition, they can also be used to increase
CC meat, egg, sperm and milk production in animals. One possible method of
XX use is by gene therapy
XX
SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 3; Length 554;
Best Local Similarity 35.4%; Pred. No. 2.8e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;
QY 6 AILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
Db 3 ATLATLAVLALATAV-----QSDSRARIVCFNSNMAVYRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDYKYTIQVFPYQDDNHNSEKRGYERFNNLRKLNKLPBELTMTISLGGWYEGSE 124
Db 56 IYSPFIVTEGNSVLIIDPELD-----VDKNGFRNFTSLRSSHPVSKFVAVGWAEGSS 110
QY 125 KYSDMAANPTYRQOQFIQSVLDLFLQYKFDGLDWEYPGSR-LGNPKIDKQNYLALVREL 183
Db 111 KYSHVAKSTRMSTIRSVSPKDYDFDGLDWEYFGAADRGGFSDDKFLYLVQEL 170
QY 184 KDAF--EPHYLLTAAPFGKDKIDRAYDIKELNKLFDMMVMYTDYHGGWENFGHNP 241
Db 171 RRAFIRVKGWELTAAPVLANPRLMEGYHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPEDELTHYFNNVTHYLYNNGATRDKLVGVPFPGYGRAWSIED----- 290
Db 231 LYKRPHD-QWAYEKLNVNDGLHLWEKGCPSNKLVGIPFYGRSFTLSAGNNYVGLGTFI 289
QY 291 RSKJLKGDPKAGMSPPGFISGEEVLSYELCQFQKEE--WHIQDYRYNAPYGYNDKI 348
Db 290 NKEAGGDPAPYTNATG-----WAYVEICTEVDKDDSGWTKKWDQKCPYAYKGTQ 342
QY 349 WGYDDLASISCKLAFKELGVSGVMVMSLENDPFKHCQKPKNPLLNKVNHWINGDEKNS 408
Db 343 WGYEDPRSVEIKMWIKQKGLGAMTAIDMDDFQGLCGEKNLIKILHKNMS----- 396
QY 409 PECILGPSHTTPTPTPTPTPT-----TPTTTPS-----PTTPTTPTPTPTPTTSP 456
Db 397 -----SYTVPPPHENTTPTPEWARPPSPDSEGDPIPTTTTAKPASTTKTKTKVT 449
QY 457 TPTPTTPTPTPT-----PTP-TTPTPAFTTSPSTTPTTHTSETPKYTVYVDGHLI 505
Db 450 TTTTAKPQSVIDEENDINVRPEKPEQPEVEVP-PTENE-----VDGSEI 497
QY 506 KYKEGD-IPHTNTHKYLVCSEFVNGWVHMPCPGTIWCQELTC 552
Db 498 -CNSDQYIPDKKCHDKYWRG--VNGE--AMQFSCQHGTVFVNLNVC 540
RESULT 15
ABP72619
ID ABP72619 standard; protein; 554 AA.
XX
AC ABP72619;
XX

DT 11-JUN-2003 (first entry)
XX Manduca sexta chitinase.
XX
KW Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
KW neuropeptide; transgenic plant; crop protection.
XX
OS Manduca sexta.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..554
FT Modified-eite /label= Mature_protein
FT Modified-eite 85..88
FT Active-site /note= "Asn is N-glycosylated"
FT Modified-site 138..146
FT Modified-site 303..306
FT Modified-eite /note= "Asn is N-glycosylated"
FT Modified-eite 545..548
FT /note= "Asn is N-glycosylated"
XX
FN WO2003014150-A2.
XX
PD 20-FEB-2003.
XX
PP 06-AUG-2002; 2002WO-GB003598.
XX
PR 08-AUG-2001; 2001GB-00019274.
XX
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
XX
PI Gatehouse JA, Fitches EC, Edwards JP;
XX
XX WPI; 2003-278469/27.
XX
XX Fusion protein useful for combating insect pests, comprises a
XX translocating moiety comprising a plant protein capable of acting as a
XX carrier to translocate toxic moiety inside plant pathogen, and a toxic
XX moiety.
XX
XX Claim 7; Fig 10; 51pp; English.
XX
CC The present sequence is that of Manduca sexta chitinase. This protein can
CC be used in claimed fusion proteins of the invention. Such fusion proteins
CC comprise a translocating moiety and a toxic moiety, where the
CC translocating moiety is a plant protein (e.g. a lectin) capable of acting
CC as a carrier to translocate the toxic moiety across the gut wall of a
CC plant pathogen, and the toxic moiety is an insect-derived peptide or
CC protein capable of causing deleterious effects on growth, development,
CC reproduction or mortality in pest insects. Suitable insect peptides and
CC proteins include allatostatin, chitinase, diuretic hormone and their
CC metabolites and analogues. Polynucleotides encoding the fusion protein,
CC vectors, host cells and transgenic plants that are resistant to disease
CC are also provided. The fusion protein is target-specific, and resists
CC degradation in the insect gut
XX
SQ Sequence 554 AA;
Query Match 27.0%; Score 838.5; DB 6; Length 554;
Best Local Similarity 35.4%; Pred. No. 2.8e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;
QY 6 AILSIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
Db 3 ATLATLAVLALATAV-----QSDSRARIVCFNSNMAVYRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDYKYTIQVFPYQDDNHNSEKRGYERFNNLRKLNKLPBELTMTISLGGWYEGSE 124
Db 56 IYSPFIVTEGNSVLIIDPELD-----VDKNGFRNFTSLRSSHPVSKFVAVGWAEGSS 110
QY 125 KYSDMAANPTYRQOQFIQSVLDLFLQYKFDGLDWEYPGSR-LGNPKIDKQNYLALVREL 183

Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 170
111 KYSHVAKSTKMSFIRSVVSEFKKYDFDGLDWEYPGAADRGGSFSDKOKFLYVQEL 170
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 241
184 KDAF--EPHGYLLTAASPGDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 241
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 230
171 RRAFIRVKGWELTAAPLANFRLMEGHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 290
242 LYKRDEDELHTYFNVNVTMHYLLNNGATRDKLVGVFPFYGRAWSIED----- 290
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 289
231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGPCSNKLVGIPFYGRSFTLSAGNNNYGLGTFI 289
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 348
291 RSKLXGDPKMSPPGFISGEEVLSYIELCOLPQKEE--WHIQYDEYNAPIGYNDKI 348
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 342
290 NKEAGGGPAPYTNATGF-----WAYEICTEVDKDDSGWTCKWDEQGCPCYAYKTQ 342
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 408
349 WVGYYDLASISCKLAFKELGVSVWVWSLENDFKHCGKPKNPLLNKVNHNINGDEKNS 408
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 396
343 WGYEDPRSVEIKMWIKQKGYLGAMTWAIDMDDFQGLCGEKKNPLIKILHKMS----- 396
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 456
409 FECILGPSTTTPTTPTPT-----TTPTPS-----PTTPTTPTPTTPTTPTSP 456
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 449
397 -----SYTVPPPHENTTTPPEWARPPSTPSDESGDPIPTTTAKPASTTKTKTKT 449
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 505
457 TTPTTPTSPPT-----PTP-TTTPAPTSTPTSTPTTTEHTSETPKYTYVDGHLI 505
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 497
450 TTTTAKPPQSVIDEENDINVRPEPKPEPEVEVP-PTENE-----VDGSEI 497
QY ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 552
506 KCYKEGD-IPHPNTNIHKYLVCFVNGWVWHIMPCPPGTIMCQEKLT 552
Db ||| | : | ||:|: ||:| ||||| ||||: | ||:| ||:| 540
498 -CNSDQDIYIPDKKHCDKYWC--VNGE--AMQFSCQHGTVFNVELNVC 540

Search completed: March 31, 2006, 15:04:01
Job time : 198 secs

RESULT 9

I38605
Oviductal glycoprotein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C:Accession: I38605
R:Arias, E.B.; Verhage, H.G.; Jaffe, R.C.
Biol. Reprod. 51, 685-694, 1994
A:Title: Complementary deoxyribonucleic acid cloning and molecular characterization of a
A:Reference number: I38605; MUID:95119256; PMID:7819450
A:Accession: I38605
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-654 <RES>
A:CROSS-references: UNIPARC:UPI000017C2DA; EMBL:U09550; NID:G529147; PID:G529148

Query Match 21.5%; Score 668; DB 2; Length 654;
Best Local Similarity 33.1%; Pred. No. 8.4e-34;
Matches 176; Conservative 91; Mismatches 192; Indels 72; Gaps 19;

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QY 10 IMACIGLMNASIKRDHNDYKSNPMRIVCYVGTWSVYHKVDPTI--EDIDPKCTHLMYG 67
Db 4 LLUWGLV---LVLRKHDAH--KLVCYFTNWA-HSRPGASILPHDLDPFLCTHLIFA 57
QY 68 FAKIDYKYTIQVDFPDYQDDNHSWEKRGYERFNNLRKNPELTTMISLGGWYEGSEKYS 127
Db 58 FASMNNOI---VAKDLQD-----EKILYPEFKLKERNRELKTLISLGGWNGFSTRT 108
QY 128 DMAANTYQQFTQSVLDLQYKFDGLDWEYPGSRGNPKIDKQNYLALVRELKDAF 187
Db 109 TMLSTPANREKFTASVISLRTHDPLGLDFLLYPLGLR-GSPMHDRAWTEFLIEELLFAP 167
QY 188 EPHG-----VLLTAASPGDKIDRAYDIKELNKLPMVMVMTYDHYGHNFYGNA 240
Db 168 RKEALLTMRPLLSSAASGVPHIVQTSYDVFLGLDLDFINVLSDHLGSEWERTGHSN 227
QY 241 PLYKRPDEDELHTFVNVTMHHYLLNNGATDKLVGMVFPFYGRAWSIEDRSKLGIDPA 300
Db 228 PLFSLPEDEPK-----SSAYAMNYWRKLGAPSEKLMIGTPYGRFRLKASKNGLOARA 281
QY 301 KGMSPPGFTSGEGVLSYIELCOLF--QKEWHIQYDEYNNAPYGVNDKIWGYDDLASI 358
Db 282 IGPASPGKYTKOEGFLAYFEICSFVWGAKKHW----IDYQYVPYANKGKWEVGYDNAISF 337
QY 359 SKCLAFKELGVGMVMSLENDDFKG-HCGP-KNPLLNKVNMMINGDEKNSFECILGPS 416
Db 338 SYKAWFIRREHFGGAMVMTLDMDVVRGTCGTPGPFPLVYVLDILVRAEFS-----S 389
QY 417 TTTPT--PTTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 466
Db 390 TSLPQWLSAANSSTDERLAVTTAWTDSKILPPGGEAGVTEHGKCNWTTTPRGT 449
QY 467 TPTPTPT-----PAPTSTPSPTTTEHTSETP--KYTTYVDGH 503
Db 450 TVTPTKETVSLGKHTVALGEKTEITGAMTMTSVGHQMTFGEKALTPV-GH 499
```

RESULT 10

A49562
Cartilage glycoprotein gp39 precursor - human
N:Alternate names: 39K synovial protein
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A49562; S10677; A33162
R:Hakala, B.E.; White, C.; Recklies, A.D.
J. Biol. Chem. 268, 25803-25810, 1993
A:Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and
A:Reference number: A49562; MUID:94064658; PMID:8245017
A:Accession: A49562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <HAK>
A:CROSS-references: UNIPROT:P36222; UNIPARC:UPI0000126C19; GB:M80927; NID:G348911; PIDN:

R:Nyirkos, P.; Golds, E.E.

Biochem. J. 269, 265-268, 1990

A:Title: Human synovial cells secrete a 39 kDa protein similar to a bovine mammary pro

A:Reference number: S10677; MUID:90328983; PMID:2375755

A:Accession: S10677

A:Molecule type: protein

A:Residues: 22-40, 'X', 42-45 <NY2>

A:CROSS-references: UNIPARC:UPI0000175A9E

C:Superfamily: Streptomyces chitinase chi40

C:Keywords: cartilage; extracellular protein; glycoprotein

F1-21/Domain: signal sequence #status predicted <SIG>

F122-383/Product: cartilage glycoprotein gp39 #status predicted <MAT>

Query Match 21.3%; Score 662; DB 2; Length 383;
Best Local Similarity 34.9%; Pred. No. 9.8e-34;
Matches 144; Conservative 81; Mismatches 136; Indels 52; Gaps 12;

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QY 2 KTIYAILSIMACIGLMNASIKRDHNDYKSNPMRIVCYVGTWSVYHKVDPTIET-IDPEK 60
Db 7 QTGFVVVLQCC-----SAYKLVCYITSNSQYREGDSCFPDALDREL 50
QY 61 CTHLMYGAFTDEYKYTIQVDFPDYQDDNHSWEKRG---YERFNNLRKNPELTTMISIG 117
Db 51 CTHIITSFANI-----SNHDITWEMNDVTLYGLMLNTLKNRPNPLKTLISVG 97
QY 118 GWYEGSEKYSDMAANTYRQOPIQSVLDLQYKFDGLDWEYPGSRNLGNPKIDKONYL 177
Db 98 GWNFSQSRFSKIATNSQKRTFIKSPVPLRTHGFDGLDLAWLYPERR-----DKQHT 151
QY 178 ALVRELKDAF----EP--HGVLITAAVSPGDKIDRAYDIKELNKLPMVMVMTYDHYGCG 231
Db 152 TLIKEMKAEFIKEAQPCKQLLSAALSAGKVTIDSSYDIKISQHLDFISITMYDFHGA 211
QY 232 WENFYGHNAPLYKRPDEDELHTFVNVTMHHYLLNNGATDKLVGMVFPFYGRAWSIEDR 291
Db 212 WRGTTGHSPLF-RQEDASPDFRFSNTDYAVGYMLRLGAPASKLVGMGTFGRSFTLAS- 269
QY 292 SKLGLDPAKGMSPGFTSGEGVLSYIELCOLFQKEWHIQYDEYNNAPYGVNDKIWVG 351
Db 270 SETGVGAFISGPGIPGRFTKEAGTLAYEICDLRGATVHRTLQG--QVPYATKGNQWVG 327
QY 352 YDDLASISCKLAFKELGVGMVMSLENDDFKG-HCGP--KNPLLNKVNMMI 401
Db 328 YDDQESVSKVQYLKDRQLAGAWWALDLDLDFQGSFCQDLRPFPLTNAIKDAL 380
```

RESULT 11

S51327
Heparin-binding glycoprotein 38K - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S51327
R:Shackleton, L.M.; Mann, D.M.; Millie, A.J.T.
submitted to the EMBL Data Library, January 1995
A:Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in diffe
A:Reference number: S51327
A:Accession: S51327
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <SHA>
A:CROSS-references: UNIPROT:Q29411; UNIPARC:UPI0000088CC8; EMBL:247803; NID:G634097; P
C:Superfamily: Streptomyces chitinase chi40

Query Match 20.9%; Score 650; DB 2; Length 383;
Best Local Similarity 36.6%; Pred. No. 5.4e-33;
Matches 139; Conservative 77; Mismatches 130; Indels 34; Gaps 11;

```
QY 34 RIVCYVGTWSVYHKVDPTIET-IDPKCTHLMYGPAKIDYKY-TIQVDPYQDDNHS 91
Db 23 KLVCIYTSWSQYREGDSCFPDAIDPLCTHIITSPANISNNEIDTLE----- 70
QY 92 W-EKRGYERFNNLRKNPELTTMISLGGWYEGSEKYSDMAANTYRQOPIQSVLDLQY 150
```

Db 71 WNDVTLDTLNTLKNRNPNTLLSVGGWNGFSQSFKSIANTQSRRTFIKSVPPFLRTH 130
Qy 151 KFDGLDLWDVEYGGSLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASVSPGKDK 204
Db 131 GFDGLDLAWISPGRR-----DKRHLTTLVKEMKAEFVREALPGTERLLLSGAVSAGKVA 184
Qy 205 IDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNAPLYKRPDDELTHTFYNNVYTHY 264
Db 185 IDRGYDIAQISQHLDFISLLTYDFHGAWRQTTHHSPFLFRQGQDASS--DRFSNADYAVSY 243
Qy 265 YLNGATRDKLVMGVPPFVGRAWSEDRSKLKLGDPAKGMSPPGFTISGEGVLSYIELCOL 324
Db 244 VRLGAPANKLVMGILPTFGRSFTLAS-SKTDVGAPASGPGIPGRFTKEKGLIAYEICDF 302
Qy 325 FQKEEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLKELGVSVMVMSLENDDDFK 384
Db 303 LOGAT--VRRPLGQQVPYATGNQWVGYYDDQESVKNKAKYLKSRQLAGAMVWTLDDLDDFR 360
Qy 385 GH-CGP--KNPLLNKVHMI 401
Db 361 GNFCQNLRFPLTSAIKOVL 380

RESULT 12

S61551
breast-regressing protein brp39 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S61551; S61550; I48271
R:Morrisson, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A:Title: neu and ras initiate murine mammary tumors that share genetic markers generally
A:Reference number: I48271; MUID:95060797; PMID:7970700
A:Accession: S61551
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-405 <MOR1>
A:CROSS-references: UNIPARC:U0100002841D; EMBL:X93035; NID:g1085065; P1
R:Morrisson, B.W.
submitted to the EMBL Data Library, November 1995
A:Reference number: S61550
A:Accession: S61550
A:Molecule type: mRNA
A:Residues: 1-245, 'I', 247-330, 'H', 332-350, 'MWALDLDFQGTQCPKEFPPLTNAIKDALA' <MOR2>
A:CROSS-references: UNIPARC:U0100002841D; EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; E
A>Note: the differences at the carboxyl end are due to a frameshift error
C:Genetics:
A:Gene: brp39
C:Superfamily: Streptomyces chitinase chi40
F:22-405/Product: breast-regressing protein brp39 #status predicted <MAT>

Query Match 20.8%; Score 646.5; DB 2; Length 405;
Best Local Similarity 34.4%; Pred No. 9.6e-33;
Matches 140; Conservative 73; Mismatches 129; Indels 65; Gaps 12;

Qy 34 RIVCYVTWSVYHK-VDPYTIIDIDPFKCTHLMYGFAKIDEXYKTIQVDFPDQDDNHSW 92
Db 23 KLVCYFTSWSQREGVGSFLDPAIQPFLCTHIYSFANIS-----SDNMLSTW 70
Qy 93 E---KRGYERFNRLKNPELTMISLGGWYSGSEKYSMDAANPTYRQFTOSVLDLFLQE 149
Db 71 EMNDESNDYDKLNKLTNTNLKTLISVGGWKGKRFSEIASNTERRTAFVRSVAPFLRS 130
Qy 150 YKFDGLDLWDVEYGGSLGNPKIDKQNYLALVRELKDAF----EP--HGVLTLTAASVSPGKD 203
Db 131 YGFDGLDLAWLYPLRL-----DKQYFTLILKELNAEFKEVQPGREKLLISAAALSAGKV 184
Qy 204 KIDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNAPLYKRPDDELTHTFYNNVYTHY 263
Db 185 AIDTGYDIAQIAHLDFINLMTYDFHGVWRQITGHHSPLFQKQDT-RFDRSYNNVAVQ 243
Qy 264 YLNGATRDKLVMGVPPFVGRAWSEDRSKLKLGDPAKGMSPPGFTISGEGVLSYIELCQ 323

Db 244 YMTRLGAQAKLMLGIPTFKGSFTLAS-SENQIGAPISGEGLPGRFTKEAGTLLAYEICD 302
Qy 324 LFOKEEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLKELGVSVMVMSLE 379
Db 303 FLKGAEVHRLSNE--KVPPATKGNQWVGYYDDQESVKNKAKYLKSRQLAGAMVWTLDDLDDFR 359
Qy 380 NDDPKGHGCGKPNPLLNKVHNMINGDEKNSPECILGPSTPTPTPTTP 426
Db 360 ----SGHCQPKN-----SSRSPTPSRMP 378

RESULT 13

S27879
secretory protein YM-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S27879
R:Chang, N.C.A.; Liu, C.H.; Chang, A.C.
submitted to the EMBL Data Library, June 1992
A:Description: Molecular characterization of a secretory protein (YM-1) transiently exp
A:Reference number: S27879
A:Accession: S27879
A:Molecule type: mRNA
A:Residues: 1-399 <CHA>
A:CROSS-references: UNIPROT:O35744; UNIPARC:U010000175AA0; EMBL:M94584; NID:g202441; P1
C:Superfamily: Streptomyces chitinase chi40
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-399/Product: secretory protein YM-1 #status predicted <MAT>

Query Match 19.6%; Score 608; DB 2; Length 399;
Best Local Similarity 36.3%; Pred. No. 2.3e-30;
Matches 141; Conservative 67; Mismatches 140; Indels 40; Gaps 14;

Qy 34 RIVCYVTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKI--DEYKTYIQVDFPDYQDDNHN 90
Db 23 QLMCYTYSWAKDRPIEGSPFEGNIDPCLCTHLYAFAGMQNNEITYT-----H 70
Qy 91 SWEKRYGERFNNLR-LKNPELTMISLGGWYSGSEKYSMDAANPTYRQFTOSVLDLFLQE 149
Db 71 EQDLRDYEALNGLKKNLTLLAIGWKNKFGPAPSAMVSTPQNRQIFQSVIRELRQ 130
Qy 150 YKFDGLDLWDVEYGGSLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASVSPGK 202
Db 131 YNFDGLNLDWQYPSGR-GSPPKDKHLSVLKEMKAFEESEVKOTPRLLLT---STGA 186
Qy 203 DKIDRAYD-IKELN--KLFDMMNMVMTYDHYGGWENFYGHNAPLYKRPDDELTHTFYNNV 259
Db 187 GIIDVIKSGTSLNCLSLDYIQWVTYLDHPDKGYTGENSEPLYKSPYDIKG-SADLNVD 245
Qy 260 YTMHYLLNNGATRDKLVMGVPPFVGRAWSEIDRSKLGKLDPAKGMSPPGFTISGEGVLSYI 319
Db 246 SIISYWKDHGAASEKLIWGPAYGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYY 305
Qy 320 ELCCQLFQK---EEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLKELGVSVMVW 376
Db 306 EVCTFLNEGATEVW----DAQEVPIAYQGNNEWVGVNVRSFKLKAQKLDNNLGGAVVW 361
Qy 377 SLENDDFPKG-HCGPKN-PLLNKVHNMNIN 402
Db 362 PLDMDDFGSGFCHQRHFPILTSLKGLDN 389

RESULT 14

A38221
chitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
C:Species: Brugia malayi
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A38221
R:Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A:Title: Transmission-blocking antibodies recognize microfilarial chitinase in brugian
A:Reference number: A38221; MUID:92179220; PMID:1542646

[illegible]

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:42:20 ; Search time 167 Seconds
(without alignments)
1388.594 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 35

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	555	US-10-218-743-15	Sequence 15, Appl
2	555	100.0	555	US-10-218-743-18	Sequence 18, Appl
3	536	96.6	536	US-10-218-743-21	Sequence 21, Appl
4	64	11.5	490	US-10-218-743-41	Sequence 41, Appl
5	64	11.5	509	US-10-218-743-35	Sequence 35, Appl
6	64	11.5	509	US-10-218-743-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909

; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match 100.0%; Score 555; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYVAILSIMACIGLMNASIKRDHNDYSKPMRIVCVGTWVYHKVDPTIEDIDPPK 60
DB 1 MKTIYVAILSIMACIGLMNASIKRDHNDYSKPMRIVCVGTWVYHKVDPTIEDIDPPK 60
QY 61 CTHLMYGFPAKIDEXYKTIQVFPDQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
DB 61 CTHLMYGFPAKIDEXYKTIQVFPDQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
QY 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSLGNPKIDKQNYLALV 180
DB 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSLGNPKIDKQNYLALV 180
QY 181 RELKDAPEPHGYLLTAAYSPGKDKIDRAYDIKELNKLFDMMNVMYDYHGGWENFYGHNA 240
DB 181 RELKDAPEPHGYLLTAAYSPGKDKIDRAYDIKELNKLFDMMNVMYDYHGGWENFYGHNA 240
QY 241 PLYKRPDETDLHTYFVNNYTHMYLNNNGATRDKLVMGVPFYGRAWSEIDRSKLGDPGA 300
DB 241 PLYKRPDETDLHTYFVNNYTHMYLNNNGATRDKLVMGVPFYGRAWSEIDRSKLGDPGA 300
QY 301 KGMSPPGFIISGEGVLSYIELCOLFQKEEMHIQDYENYAPYGYNDKLVWGVDDDLASISC 360
DB 301 KGMSPPGFIISGEGVLSYIELCOLFQKEEMHIQDYENYAPYGYNDKLVWGVDDDLASISC 360
QY 361 KLAFLKEIGVSGVMVMSLENDDEKHCCKPKNKLKVNMMINGDEKNSFECILGSTTTP 420
DB 361 KLAFLKEIGVSGVMVMSLENDDEKHCCKPKNKLKVNMMINGDEKNSFECILGSTTTP 420
QY 421 TPTT 480
DB 421 TPTT 480
QY 481 TSPPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCEFYNGGWWHIMP 540
DB 481 TSPPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCEFYNGGWWHIMP 540
QY 541 PGTWCQKLTICGE 555
DB 541 PGTWCQKLTICGE 555

RESULT 2

US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13

	; PRIOR APPLICATION NUMBER:	US/09/292,225	
	; PRIOR FILING DATE:	1999-04-15	
	; PRIOR APPLICATION NUMBER:	60/098,909	
	; PRIOR FILING DATE:	1998-09-02	
	; PRIOR APPLICATION NUMBER:	60/085,295	
	; PRIOR FILING DATE:	1998-05-13	
	; PRIOR APPLICATION NUMBER:	60/098,565	
	; PRIOR FILING DATE:	1998-04-17	
	; PRIOR APPLICATION NUMBER:	09/062,013	
	; PRIOR FILING DATE:	1998-04-17	
	; NUMBER OF SEQ ID NOS:	49	
	; SOFTWARE:	PatentIn Ver. 2.0	
	; SEQ ID NO 18		
	; LENGTH:	555	
	; TYPE:	PRT	
	; ORGANISM:	Dermatophagoides farinae	
	US-10-218-743-18		
	Query Match	100.0%; Score 555; DB 4; Length 555;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 555; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 MKTIIAILSLMACIGLMNASTIKRHDNDYSKNPMRIVCYVGCTWSVYHKVDPTIEDIDPFK	60	
Qy	61 CTHLMYGFAKIDEKYTIQTVPDPPQDDNNHNSWEKRGYERFNNRLKNPELTTMISLGWY	120	
Db	61 CTHLMYGFAKIDEKYTIQTVPDPPQDDNNHNSWEKRGYERFNNRLKNPELTTMISLGWY	120	
Qy	121 EGSEKYSDMAANTPYROQFIQSVLDFLOEYKFPGDLDMWEYPGSR LGNPKIDKQNYLAIV	180	
Db	121 EGSEKYSDMAANTPYROQFIQSVLDFLOEYKFPGDLDMWEYPGSR LGNPKIDKQNYLAIV	180	
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Db	181 RELKOAFEPHGYYLLTAAVSPGDKLDRA YDI K E L N K L F D W N V M T Y D H G G W E N P Y G H N A	240	
Qy	241 PLYKRPDETDELHTYTFNVNTMYHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA	300	
Db	241 PLYKRPDETDELHTYTFNVNTMYHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA	300	
Qy	301 KGMSPPGFISGEEGVLSYIELCOLPQEKEWHIQYDEYYNAPYGYNDKI WVGYDDLASISC	360	
Db	301 KGMSPPGFISGEEGVLSYIELCOLPQEKEWHIQYDEYYNAPYGYNDKI WVGYDDLASISC	360	
Qy	361 KLAFLEKGVSQVMVWSLENDDFKHCPCPKPLLNKVGNMIMGDBEKSGFECLIGBSTTTP	420	
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Qy	421 TPPTTPPT	480	
Db	421 TPPTTPPT	480	
Qy	481 TPSPTTTEHTSETPKTYTYTVDGHLIKCYKEGDIPHPNTNIHKYLVCSEFVGGWWHIMCP	540	
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Db	541 PGTIWCQCKLTTCIGE 555		

RESULT 4
US-10-218-743-41
; Sequence 41. Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3

; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-41

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Best Local Similarity 100.0%; Pred. No. 1.6e-54; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0;
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DB 292 GEGVLSYIELCOLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLGLV 351
QY 371 SGVM 374
DB 352 SGVM 355

RESULT 5

US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35

Query Match 11.5%; Score 64; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-54; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0;
QY 311 GEGVLSYIELCOLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLGLV 370
DB 311 GEGVLSYIELCOLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLGLV 370
QY 371 SGVM 374

DB 371 SGVM 374
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RESULT 6

US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38

Query Match 11.5%; Score 64; DB 4; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.6e-54; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0;
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DB 311 GEGVLSYIELCOLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFKLGLV 370
QY 371 SGVM 374
DB 371 SGVM 374

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:08:21 ; Search time 48 Seconds
(without alignments)
955.938 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/aaa/H COMB.pap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3107	100.0	555	2	US-09-292-225-18
3	3014	97.0	536	2	US-09-292-225-21
4	2542	81.8	509	2	US-09-292-225-35
5	2542	81.8	509	2	US-09-292-225-38
6	2475	79.7	490	2	US-09-292-225-41
7	838.5	27.0	554	1	US-08-524-051-2
8	838.5	27.0	554	2	US-09-052-778-16
9	815.5	26.2	583	2	US-09-545-814-2
10	815.5	26.2	583	2	US-09-545-814-5
11	812.5	26.2	635	2	US-09-545-814-32
12	811.5	26.1	559	2	US-09-545-814-14
13	738	23.8	466	1	US-08-486-839-4
14	738	23.8	466	2	US-09-151-011-4
15	738	23.8	466	2	US-09-039-198A-2
16	738	23.8	466	2	US-09-343-623-4
17	738	23.8	466	2	US-08-877-599-2
18	738	23.8	466	2	US-09-267-574-2
19	738	23.8	466	2	US-09-977-827-4
20	737.5	23.7	520	2	US-10-268-919-3
21	732.5	23.6	387	1	US-08-486-839-6
22	732.5	23.6	387	2	US-09-151-011-6
23	732.5	23.6	387	2	US-09-343-623-6
24	732.5	23.6	387	2	US-09-977-827-6
25	732	23.6	466	2	US-09-039-198A-4
26	732	23.6	466	2	US-08-877-599-4
27	732	23.6	466	2	US-09-267-574-4

28	721.5	23.2	373	2	US-09-039-198A-14	Sequence 14, Appl
29	721.5	23.2	373	2	US-09-039-198A-15	Sequence 15, Appl
30	721.5	23.2	373	2	US-08-877-599-14	Sequence 14, Appl
31	721.5	23.2	373	2	US-08-877-599-15	Sequence 15, Appl
32	721.5	23.2	373	2	US-09-267-574-14	Sequence 14, Appl
33	721.5	23.2	373	2	US-09-267-574-15	Sequence 15, Appl
34	708.5	22.8	455	2	US-10-130-158A-1	Sequence 1, Appl
35	708.5	22.8	476	2	US-10-130-158A-5	Sequence 5, Appl
36	708.5	22.8	476	2	US-10-268-919-5	Sequence 5, Appl
37	672.5	21.6	489	2	US-09-545-814-29	Sequence 29, Appl
38	669	21.5	682	2	US-09-949-016-10624	Sequence 10624, A
39	662	21.3	383	2	US-09-949-016-6053	Sequence 6053, Ap
40	658	21.2	365	2	US-09-949-016-7947	Sequence 7947, Ap
41	650	20.9	383	2	US-09-459-749D-17	Sequence 17, Appl
42	640.5	20.6	377	2	US-10-130-158A-18	Sequence 18, Appl
43	640.5	20.6	398	2	US-10-130-158A-17	Sequence 17, Appl
44	632	20.3	396	2	US-09-949-016-8736	Sequence 8736, Ap
45	630	20.3	385	1	US-08-694-915-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-15

; Sequence 15, Application US/09292225

; Patent No. 6455586

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine A.

; APPLICANT: Hunter, Shirley Wu

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: AL-2-C3

; CURRENT APPLICATION NUMBER: US/09/292,225

; CURRENT FILING DATE: 1999-04-15

; EARLIER APPLICATION NUMBER: 60/098,909

; EARLIER FILING DATE: 1998-09-02

; EARLIER APPLICATION NUMBER: 60/085,295

; EARLIER FILING DATE: 1998-05-13

; EARLIER APPLICATION NUMBER: 60/098,565

; EARLIER FILING DATE: 1998-04-17

; EARLIER APPLICATION NUMBER: 09/062,013

; EARLIER FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 555

; TYPE: PRT

; ORGANISM: Dermatophagoides farinae

US-09-292-225-15

Query Match 100.0%; Score 3107; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCVGTWTSVYHKVDPTIEDIDPFK	60
Qy	61	CTHLMYGFPAKIDEXKYTIQVDPDYQDDNHNSWEKRGYERFNNLRKKNPDLTMTISLGGM	120
Db	61	CTHLMYGFPAKIDEXKYTIQVDPDYQDDNHNSWEKRGYERFNNLRKKNPDLTMTISLGGM	120
Qy	121	EGSEKYSDMAANPTTQOFTIOSVLDLDFLOEYKFDGLDLDWEYPGSRLGNPKDKQNYLALV	180
Db	121	EGSEKYSDMAANPTTQOFTIOSVLDLDFLOEYKFDGLDLDWEYPGSRLGNPKDKQNYLALV	180
Qy	181	RELKDAPEPHGYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVTYDVGWENPYGHNA	240
Db	181	RELKDAPEPHGYLLTAASVPGKDKIDRAYDIKELNKLFDWMNVTYDVGWENPYGHNA	240
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Db 241 PLYKRPDETDLHTYFNNVYTHYYLNNGATRDKLVGMVGFYGRAWSIEDRSKLGDP 300
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Db 301 KGMSPPGFISGEGVLSYIELCQLFQKEBWHIQYDEYNNAPYGYNDKIWVGVDLASC 360
Qy 361 KLAFLKELGVSVMVMSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPTTTP 420
Db 361 KLAFLKELGVSVMVMSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPTTTP 420
Qy 421 TPPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 480
Db 421 TPPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 480
Qy 481 TPSPTTHTSTPKYTYVDGHLIKCYKEGDI PHTNHNKYLVCVFVNGGWWHIMPCP 540
Db 481 TPSPTTHTSTPKYTYVDGHLIKCYKEGDI PHTNHNKYLVCVFVNGGWWHIMPCP 540
Qy 541 PGTWCQEKLTICGE 555
Db 541 PGTWCQEKLTICGE 555
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RESULT 2

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US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18
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Query Match 100.0%; Score 3107; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.2e-239; Mismatches 0; Indels 0; Gaps 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKTIYAILSIMACIGLNNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYIEDIDPFK 60

Qy 61 CTHLMYGFPAKIDYKYTIQVFPYQDDNHNNSWEKRGYERFNNLRLKNPELTMTISLGWY 120
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Qy 121 EGSEKYSMAAAPTTRQOPIQSVLDFQYKFDGLDWEYPGSLGNPKIDKQNYLALV 180
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Qy 181 RELKDAFEPHGYLLTAASVPGDKIDRAYDIKELNKLFDMMNVMTYDYGHWENFYGHNA 240
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Qy 301 KGMSPPGFISGEGVLSYIELCQLFQKEBWHIQYDEYNNAPYGYNDKIWVGVDLASC 360
Db 301 KGMSPPGFISGEGVLSYIELCQLFQKEBWHIQYDEYNNAPYGYNDKIWVGVDLASC 360
Qy 361 KLAFLKELGVSVMVMSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPTTTP 420
Db 361 KLAFLKELGVSVMVMSLENDDFKGHCQPKNPLLNKVNHNMGDEKNSFECILGPTTTP 420
Qy 421 TPPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 480
Db 421 TPPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 480
Qy 481 TPSPTTHTSTPKYTYVDGHLIKCYKEGDI PHTNHNKYLVCVFVNGGWWHIMPCP 540
Db 481 TPSPTTHTSTPKYTYVDGHLIKCYKEGDI PHTNHNKYLVCVFVNGGWWHIMPCP 540
Qy 541 PGTWCQEKLTICGE 555
Db 541 PGTWCQEKLTICGE 555
```

RESULT 3

```
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21
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Query Match 97.0%; Score 3014; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 3e-232; Mismatches 0; Indels 0; Gaps 0;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 SIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYIEDIDPFKCTHLMYGFPAKIDYKYTIQ 79
Db 1 SIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYIEDIDPFKCTHLMYGFPAKIDYKYTIQ 60

Qy 80 VFDPYQDDNHNNSWEKRGYERFNNLRLKNPELTMTISLGWYEGSEKYSDMAANPTTRQOF 139
Db 61 VFDPYQDDNHNNSWEKRGYERFNNLRLKNPELTMTISLGWYEGSEKYSDMAANPTTRQOF 120

Qy 140 IQSVLDFLOEYKFDGLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASV 199
Db 121 IQSVLDFLOEYKFDGLDWEYPGSLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASV 180

Qy 200 PGDKIDRAYDIKELNKLFDMMNVMTYDYGHWENFYGHNAPLYKRPDETDLHTYFNNV 259
Db 181 PGDKIDRAYDIKELNKLFDMMNVMTYDYGHWENFYGHNAPLYKRPDETDLHTYFNNV 240
```

QY 260 YTMHYLLNNGATRDKLVGMGPVGYGRAWSIEDRSKLGDPAGKMGSPGGFISGEEGLSVI 319
Db 241 YTMHYLLNNGATRDKLVGMGPVGYGRAWSIEDRSKLGDPAGKMGSPGGFISGEEGLSVI 300
QY 320 ELCQLFQKEEMHIQYDEYNNAPYGYNDKIWVGYYDLASISCKLAFKELGVSVMVWSLE 379
Db 301 ELCQLFQKEEMHIQYDEYNNAPYGYNDKIWVGYYDLASISCKLAFKELGVSVMVWSLE 360
QY 380 NDDFKHCGKQKPLLNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT 439
Db 361 NDDFKHCGKQKPLLNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT 420
QY 440 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 499
Db 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 500 VDGLHIKCYKEGDIHPHTNIHKYLVCEFYNGGVMVHIMPCPPGTIWCQEKLTICIG 555
Db 481 VDGLHIKCYKEGDIHPHTNIHKYLVCEFYNGGVMVHIMPCPPGTIWCQEKLTICIG 536

RESULT 4

US-09-292-225-35
; Sequence 35, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; TYPE: PRT
; LENGTH: 509
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35

Query Match 81.8%; Score 2542; DB 2; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.3e-194;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLMMASIKRDNDYSKPMRIVCYVGTWSVVKVDPTTIEDIDPPK 60
Db 1 MKTTFALFCIWACIGLMMNAATKRDNNYSKPMRIVCYVGTWSVVKVDPTTIEDIDPPK 60
QY 61 CTHLMYGFPAKIDYKYTIQVDFPDYDDNNHNSWEKGYERFNNLRKLPBELTTMISLGWY 120
Db 61 CTHLMYGFPAKIDYKYTIQVDFPDYDDNNHNSWEKGYERFNNLRKLPBELTTMISLGWY 120
QY 121 EGSEKYSMAANPTTTRQOQFISVLDPLQYKFDGLDLDWEYPSGLGNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTTTRQOQFISVLDPLQYKFDGLDLDWEYPSGLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKIDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNA 240
Db 181 RELKEAFEPFGYLLTAAVSPGKIDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNA 240
QY 241 PLYKRPDETDLHTYFNVNNTMYYLLNNGATRDKLVGMGPVGYGRAWSIEDRSKLGDPGA 300

Db 241 PLYKRPDETDLHTYFNVNNTMYYLLNNGATRDKLVGMGPVGYGRAWSIEDRSKVLGDPGA 300
QY 301 KGMSPPGFISGEEGLSVIYELCOLFOKEEMHIQYDEYNNAPYGYNDKIWVGYYDLASIS 360
Db 301 KGMSPPGFISGEEGLSVIYELCOLFOKEEMHIQYDEYNNAPYGYNDKIWVGYYDLASIS 360
QY 361 KLAFLKELGVSVMVWSLENDDFKGHCGKQKPLLNKVNMMINGDEKNSFECILGSPSTTPT 420
Db 361 KLAFLKELGVSVMVWSLENDDFKGHCGKQKPLLNKVNMMINGDEKNSFECILGSPSTTPT 420
QY 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Db 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 434
QY 481 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 537
Db 435 ---PTTDDSTSETPKYTIYIDGHLIKCYKQGYLPHPTDVHKLVCYEIATPNGGVMVHIM 491
QY 538 PCPPGTIWCQEKLTICIG 555
Db 492 DCPKGTWRHATLKNCIQE 509

RESULT 5

US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
; TYPE: PRT
; LENGTH: 509
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match 81.8%; Score 2542; DB 2; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.3e-194;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLMMASIKRDNDYSKPMRIVCYVGTWSVVKVDPTTIEDIDPPK 60
Db 1 MKTTFALFCIWACIGLMMNAATKRDNNYSKPMRIVCYVGTWSVVKVDPTTIEDIDPPK 60
QY 61 CTHLMYGFPAKIDYKYTIQVDFPDYDDNNHNSWEKGYERFNNLRKLPBELTTMISLGWY 120
Db 61 CTHLMYGFPAKIDYKYTIQVDFPDYDDNNHNSWEKGYERFNNLRKLPBELTTMISLGWY 120
QY 121 EGSEKYSMAANPTTTRQOQFISVLDPLQYKFDGLDLDWEYPSGLGNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTTTRQOQFISVLDPLQYKFDGLDLDWEYPSGLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAAVSPGKIDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNA 240
Db 181 RELKEAFEPFGYLLTAAVSPGKIDRAYDIKELNKLFDMMNMVMTYDHYGGWENFYGHNA 240
QY 241 PLYKRPDETDLHTYFNVNNTMYYLLNNGATRDKLVGMGPVGYGRAWSIEDRSKVLGDPGA 300

QY 65 MYGFAKIDEXYKTIQVDPYQDDNHNHSEKRGVERFNNRLKNPELTTMISLGGWEGSE 124
DB 56 IYSFIVGTGENSEVLIDBELD-----VDKNFRNFTSLSRSHPSVKFMVAVGGWAEGBSS 110
QY 125 KYSDMAANTYRQOFTQSVLDLQBYKFDGLDLDWEYPGSR--LGNPKIDKQNYLALVREL 183
DB 111 KYSHVAAQSTRMSFIRSVVFLKYYDFDGLDLDWEYPCGAADRGGSFSDKDFLYLVQEL 170
QY 184 KDAP--EPHGYYLLTAASPGKDKIDRAYDIKELNKLFDMMNVMYTDYHGGWENFYGHNAP 241
DB 171 RRAFIRVKGWELTAAPLANFRLMEGHVHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNNVNTMHHYLLNNGATRDKLVMGVPPFYGRANSIED-----290
DB 231 LYKRPHD-QWAYEKLNVNDGLHLEWEEKGCPSPNKLVGIPFYGRSFTLSAGNNYGLGTPI 289
QY 184 KDAP--EPHGYYLLTAASPGKDKIDRAYDIKELNKLFDMMNVMYTDYHGGWENFYGHNAP 241
DB 171 RRAFIRVKGWELTAAPLANFRLMEGHVHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNNVNTMHHYLLNNGATRDKLVMGVPPFYGRANSIED-----290
DB 231 LYKRPHD-QWAYEKLNVNDGLHLEWEEKGCPSPNKLVGIPFYGRSFTLSAGNNYGLGTPI 289
QY 291 RSKLGLDPAKGMSPPGFISGEEGVLSEIQLCOLFOKEE--WHIOYDEYNNAPYGYNDKI 348
DB 290 NKEAGGDPAPYTNATG-----WAYYEICTEVDKDSGWTKKWDEQKCPYAYKGTO 342
QY 349 WGYDDLASISCKLAFKELGVLGSGVMVMSLENDDPKGGHCGPNKPLNKHNNINGDEKNS 408
DB 343 WGYEDPRSVEIKNNWIKQGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKGMS-----396
QY 409 FECILGSPSTTPTPTTPTTPT-----TTPTTPS-----PTTPTTPTPTTPTTPTSP 456
DB 397 -----SYTVPPPHHTENTTPTPEWARPPSTPSDPSGDPITPTTTAKPASTTKTIVKTT 449
QY 457 TPTPTTPTPTT-----PTP--TPTPTPTTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPT 505
DB 450 TTTAKPPQSVIDEENDINVRPEKPEQPEVEVP-PTENE-----VDGSEI 497
QY 506 KCKYKEDG-IPHTNIIHKYLCVFNGGWWHIMPCPPGTIMCOEKLTC 552
DB 498 -CNSDDYIPDKKCHDKYRWC--VNGE--AMQFSCQHGTVFNVNLCV 540

RESULT 8
US-09-052-778-16
; Sequence 16, Application US/09052778A
; Patent No. 6060590
; GENERAL INFORMATION:
; APPLICANT: Bryant, Peter J.
; APPLICANT: Kawamura, Kazuo
; TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
; FILE REFERENCE: 07306/015001
; CURRENT APPLICATION NUMBER: US/09/052, 778A
; CURRENT FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-052-778-16

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 1.4e-58;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

QY 6 AILSINACTGLMNASIKRDHNDYSKNPMRIVCVGWTWSYTHK-VDPYTTIEDIDPPKCTHLM 64
DB 3 ATLATLAVLATAV-----QSDSRARIVCFNSWAVRPGVGRYGIEDIPVEKCTHI 55
QY 65 MYGFAKIDEXYKTIQVDPYQDDNHNHSEKRGVERFNNRLKNPELTTMISLGGWEGSE 124
DB 56 IYSFIVGTGENSEVLIDBELD-----VDKNFRNFTSLSRSHPSVKFMVAVGGWAEGBSS 110
QY 125 KYSDMAANTYRQOFTQSVLDLQBYKFDGLDLDWEYPGSR--LGNPKIDKQNYLALVREL 183
DB 111 KYSHVAAQSTRMSFIRSVVFLKYYDFDGLDLDWEYPCGAADRGGSFSDKDFLYLVQEL 170

QY 184 KDAP--EPHGYYLLTAASPGKDKIDRAYDIKELNKLFDMMNVMYTDYHGGWENFYGHNAP 241
DB 171 RRAFIRVKGWELTAAPLANFRLMEGHVHVPCLQELDAIHVMSYDLRGNWAGFADVHSP 230
QY 242 LYKRPDETDELHTYFNNVNTMHHYLLNNGATRDKLVMGVPPFYGRANSIED-----290
DB 231 LYKRPHD-QWAYEKLNVNDGLHLEWEEKGCPSPNKLVGIPFYGRSFTLSAGNNYGLGTPI 289
QY 291 RSKLGLDPAKGMSPPGFISGEEGVLSEIQLCOLFOKEE--WHIOYDEYNNAPYGYNDKI 348
DB 290 NKEAGGDPAPYTNATG-----WAYYEICTEVDKDSGWTKKWDEQKCPYAYKGTO 342
QY 349 WGYDDLASISCKLAFKELGVLGSGVMVMSLENDDPKGGHCGPNKPLNKHNNINGDEKNS 408
DB 343 WGYEDPRSVEIKNNWIKQGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKGMS-----396
QY 409 FECILGSPSTTPTPTTPTTPT-----TTPTTPS-----PTTPTTPTPTTPTTPTSP 456
DB 397 -----SYTVPPPHHTENTTPTPEWARPPSTPSDPSGDPITPTTTAKPASTTKTIVKTT 449
QY 457 TPTPTTPTPTT-----PTP--TPTPTPTTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPT 505
DB 450 TTTAKPPQSVIDEENDINVRPEKPEQPEVEVP-PTENE-----VDGSEI 497
QY 506 KCKYKEDG-IPHTNIIHKYLCVFNGGWWHIMPCPPGTIMCOEKLTC 552
DB 498 -CNSDDYIPDKKCHDKYRWC--VNGE--AMQFSCQHGTVFNVNLCV 540

RESULT 9
US-09-545-814-2
; Sequence 2, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; FILE REFERENCE: PC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545, 814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-2

Query Match 26.2%; Score 815.5; DB 2; Length 583;
Best Local Similarity 34.6%; Pred. No. 1e-56;
Matches 198; Conservative 94; Mismatches 205; Indels 75; Gaps 23;

QY 7 ILSINACTGLMNASIKRDHNDYSKNPMRIVCVGWTWSYTHK-VDPYTTIEDIDPPKCTHLM 65
DB 6 LLAVLCATAISSINTV-----EASDQKARIVCFNSWAVRPGVGRYGIEDIDPVDLCTHIV 61
QY 66 YGFAKIDEXYKTIQVDPYQDDNHNHSEKRGVERFNNRLKNPELTTMISLGGWYEGSEK 125
DB 62 YSFGVDDKDSVSLVIDPELDIDDN-----GFKPNTLNRKTHPNVVKLQIAGVGAEGGK 116
QY 126 YSDMAANTYRQOFTQSVLDLQBYKFDGLDLDWEYPGSR--LGNPKIDKQNYLALVREL 184
DB 117 YSTWVAEKRSKRSFIRSVVDFMNEYKFDGFDLDWEYPCGAADRGGSFSDKDFLYVQEL 176
QY 185 DAPEPHG--YLLTAASPGKDKIDRAYDIKELNKLFDMMNVMYTDYHGGWENFYGHNAP 242
DB 177 RAFNKGQKWEITWAVPIAKPRLQSGYHVPCLQELDAIHVMSYDLRGNWAGFADHSP 236
QY 243 YKRPDETDELHTYFNNVNTMHHYLLNNGATRDKLVMGVPPFYGRANSIEDRSK-LKLG---D 298

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:00:56 ; Search time 235 Seconds
(without alignments)
1666.248 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107

Sequence: 1 MKTIYAILSLMACIGLGNAS.....IMPCPGTGWCKELKTIGCE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3107	100.0	555	2 Q9U6R7	DERFA
2	2816.5	90.7	558	2 Q4JK70	dermatophag
3	2744.5	88.3	532	2 Q4JK69	dermatophag
4	1008.5	32.5	525	2 Q44079	anopheles g
5	1006.5	32.4	525	2 Q7Q517	ANOXA
6	942	30.3	431	2 Q81SH5	ARAC
7	869	28.0	1635	2 O17412	AEDE
8	863	27.8	493	2 Q56J11	9HYME
9	854.5	27.5	4498	2 Q9W223	DROME
10	851	27.4	2083	2 Q7FWC2	ANOXA
11	847	27.3	544	2 Q9GQC4	BOMMO
12	842	27.1	476	2 Q9W2M7	DROME
13	842	27.1	2838	2 Q8MP05	TENMO
14	839	27.0	566	2 Q8WR52	BOMMO
15	838.5	27.0	554	1 CHIT	MANSE
16	837.5	27.0	467	2 O15993	PENUP
17	837.5	27.0	543	2 Q9GR93	BOMMO
18	837.5	27.0	543	2 Q9GV05	BOMMO
19	837.5	27.0	565	2 P90710	BOMMO
20	837.5	27.0	595	2 Q9VFR3	DROME
21	831.5	26.8	467	2 Q9ITU3	PENVA
22	829.5	26.7	565	2 Q9PGG9	BOMMA
23	829.5	26.7	588	2 Q9VUB9	HELAM
24	823.5	26.5	557	2 Q9MTK0	CHOFU
25	823	26.5	488	2 Q9W034	BUFJA
26	819.5	26.4	533	2 Q9QE61	TRICA
27	814.5	26.2	552	2 Q9GV44	SPOLT
28	810	26.1	574	2 O17411	AEDE
29	808	26.0	552	2 Q9EH25	SPOLT
30	802	25.8	483	2 Q23737	9HYME
31	800.5	25.8	555	2 Q9QSW1	SPOFR

32	799	25.7	471	2 Q6NZ28	BRARE
33	798	25.7	572	2 Q26042	PENJP
34	796	25.6	565	2 Q7PQX4	ANOXA
35	795	25.6	2286	2 Q7PL80	DROME
36	793.5	25.5	489	2 Q6GP67	XENLA
37	790.5	25.4	553	2 Q7Q4Y2	2NEOP
38	790	25.4	620	2 Q9Y0D4	PENMO
39	787	25.3	553	2 P91731	HYPCU
40	780	25.1	470	2 Q80387	BRARE
41	780	25.1	470	2 Q6P006	BRARE
42	776.5	25.0	456	2 Q7Q6W6	ANOXA
43	772	24.8	492	2 Q6DJ52	XENTR
44	770	24.8	484	2 Q75WB9	PAROL
45	768.5	24.7	470	2 Q4L129	9DIPT

ALIGNMENTS

RESULT 1
Q9U6R7 DERFA
ID Q9U6R7_DERFA PRELIMINARY; PRT; 555 AA.
AC Q9U6R7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 98kDa HDM allergen.
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21189488; PubMed=11292526; DOI=10.1016/S0165-2427(00)00258-0;
RA McCall C., Hunter S., Stedman K., Weber E., Hillier A., Bozic C.,
RA Rivoire B., Olivry T.;
RT "Characterization and cloning of a major high molecular weight house
dust mite allergen (Der f 15) for dogs";
RL Vet. Immunol. Immunopathol. 78:231-247(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Weber E.R., Hunter S., Stedman K., McCall C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178772; AAD52672.1; -, mRNA.
DR HSSP; Q13231; ILG2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase II.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CEM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 555 AA; 63238 MW; 0E4564A1A459B30B CRC64;

Query Match 100.0%; Score 3107; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e-166;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKTIYAILSLMACIGLGNASIKRDNDYKKNPMRIVCVGTWSYHKVDPVTIEDIDPFK 60
Db	1	MKTIYAILSLMACIGLGNASIKRDNDYKKNPMRIVCVGTWSYHKVDPVTIEDIDPFK 60
Qy	61	CTHLMYFAKIDYKYTIQVDFDPYQDDNHSWEKRGYERFNNLRKPNELTMTISLGGWY 120

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Db 121 CTHLMYGFAKIDYKYTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
Qy 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
Qy 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Qy 241 PLYKRPDDELTHTYFNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
Db 241 PLYKRPDDELTHTYFNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
Qy 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIQYDEYNNAPYGYNDKLVWGYDDLASISC 360
Db 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIQYDEYNNAPYGYNDKLVWGYDDLASISC 360
Qy 361 KLAFLKELGSGVMVMSLENDDFKGHCCKPKNPLLNKVNMMINGDEKNSFECILGPSTTTP 420
Db 361 KLAFLKELGSGVMVMSLENDDFKGHCCKPKNPLLNKVNMMINGDEKNSFECILGPSTTTP 420
Qy 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVCVFNGGWWHIMPCP 540
Db 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVCVFNGGWWHIMPCP 540
Qy 541 PGTIWCQEKLTICGE 555
Db 541 PGTIWCQEKLTICGE 555

RESULT 2
Q4JK70_DERPT
ID Q4JK70_DERPT PRELIMINARY; PRT; 558 AA.
AC Q4JK70;
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE Group 15 allergen protein.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcophormes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OC NCBI_taxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15-A chitinase allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; DQ078740; AAY84564.1; -; mRNA.
SQ SEQUENCE 558 AA; 63497 MW; 3CBFD8C829D4CEB8 CRC64;

Query Match 90.7%; Score 2816.5; DB 2; Length 558;
Best Local Similarity 89.8%; Pred. No. 3.2e-150;
Matches 503; Conservative 27; Mismatches 23; Indels 7; Gaps 4;

Qy 1 MKTYAILSIMACIGLMNASIKRDNDYKSNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
Db 1 MKTSCAILILMACFGLMNAVKRDHNNYKSNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
Qy 61 CTHLMYGFAKIDYKYTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
Db 61 CTHLMYGFAKIDYKYTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
Qy 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
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Qy 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Qy 241 PLYKRPDDELTHTYFNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
Db 241 PLYKRPDDELTHTYFNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
Qy 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIQYDEYNNAPYGYNDKLVWGYDDLASISC 360
Db 301 KGMSPPGFISGEGVLSYIELCOLFOKEWHIQYDEYNNAPYGYNDKLVWGYDDLASISC 360
Qy 361 KLAFLKELGSGVMVMSLENDDFKGHCCKPKNPLLNKVNMMINGDEKNSFECILGPSTTTP 420
Db 361 KLAFLKELGSGVMVMSLENDDFKGHCCKPKNPLLNKVNMMINGDEKNSFECILGPSTTTP 420
Qy 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVCVFNGGWWHIMPCP 540
Db 421 TPSTTTTHTSETPKYTYVDGHLIKCYKEGDI PHPTNIHKYLVCVFNGGWWHIMPCP 540
Qy 541 PGTIWCQEKLTICGE 555
Db 541 PGTIWCQEKLTICGE 555

RESULT 3
Q4JK69_DERPT
ID Q4JK69_DERPT PRELIMINARY; PRT; 532 AA.
AC Q4JK69;
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE Group 15 allergen protein short isoform.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcophormes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OC NCBI_taxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15 0102-An isoform of the gene for Der p15 encoding a chitinase allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; DQ078741; AAY84565.1; -; mRNA.
SQ SEQUENCE 532 AA; 60953 MW; A92BF86C3C6498ED CRC64;

Query Match 88.3%; Score 2744.5; DB 2; Length 532;
Best Local Similarity 88.3%; Pred. No. 3.3e-146;
Matches 490; Conservative 27; Mismatches 15; Indels 23; Gaps 4;

Qy 1 MKTYAILSIMACIGLMNASIKRDNDYKSNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
Db 1 MKTSCAILILMACFGLMNAVKRDHNNYKSNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
Qy 61 CTHLMYGFAKIDYKYTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
Db 61 CTHLMYGFAKIDYKYTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGGWY 120
Qy 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
Db 121 EGSEKYSMAANPTVROQFIQSVDLFLQYKFDGLDLDWEYPGSRIGNPKIDKQNYLALV 180
Qy 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGKIDRAYDIKELNKLFDWMNMTYDYHGGWENFYGHNA 240
Qy 241 PLYKRPDDELTHTYFNVTMYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
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Db 241 PLYKRPDETDLHTYFNVNMTTHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKVXLGDP 300
Qy 301 KMSPPGFTSGREGVLSYELCOLFQKEWHIOYDEYNAPYGYNDKIWGVYDDLASISC 360
Db 301 KMSPPGFTSGREGVLSYELCOLFQKEWHIOYDEYNAPYGYNDKIWGVYDDLASISC 360
Qy 361 KLAFUKELGVSGVMWSLENDDFKHCQPKPKNLLKNVNMINGDEKNSFECILGSPSTTP 420
Db 361 KLAFUKELGVSGVMWSLENDDFKHCQPKPKNLLKNVNMINGDEKNSFECILGSPSTTP 420
Qy 421 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 480
Db 421 TP-----TPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 457
Qy 481 TPTPTTHTSTPKYTVTVVGDHLIKCYKEGDI PHPTNIHKYLVCFEVNGGWWHIMPCP 540
Db 458 TPTPTTSTSTPKYTVTVVGDHLIKCYKEGDI PHPTNIHKYLVCFEVNGGWWHIMPCP 517
Qy 541 PGTIWCQKLCITCE 555
Db 518 PGTIWCQKLCITCE 532

RESULT 4
ID O44079 ANOGA
AC O44079 ANOGA PRELIMINARY; PRT; 525 AA.
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase.
GN Name=AgChi-1;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Gut;
RA MEDLINE=98030563; PubMed=9360958; DOI=10.1074/jbc.272.46.28895;
RX Shen Z., Jacobs-Lorena M.;
RT "Characterization of a novel gut-specific chitinase gene from the
human malaria vector Anopheles gambiae.";
RL J. Biol. Chem. 272:28895-28900(1997).
DR EMBL; AF008575; AAB87764.1; -; mRNA.
DR FIR; T44445; T44445.
DR HSSP; Q13231; ILG2.
DR Ensemble; ENSANGG00000017996; Anopheles gambiae.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase II.
DR InterPro; IPR002557; Chitin bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS05940; CHIT_BIND_II; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 525 AA; 57211 MW; 32343608BFF36165 CRC64;

Query Match 32.5%; Score 1008.5; DB 2; Length 525;
Best Local Similarity 38.4%; Pred. No. 1.1e-48;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;
Qy 8 LSIMACIGLMNASIKRD-HNDYSKNPMEIVCVGWTSVYHKVD-PYTIEDIDPFKCTHLM 65
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Db 5 VGVLVAVAAAAFAEBPHKAASAEKKVVCVGTWVYVRPGNGRYDIEHIDPSLCTHLM 64
Qy 66 YGPAKIDBYKYTIQVDFYQDDNHNSEKRGYERFNNLRKLNPELTITWISLGGWTEGSEK 125
Db 65 YGFFGINS-DATVRIIDPYLDLBN-MGRGHIKRFPVGLKNVGPGLKTLAAIGMNGEGRK 122
Qy 126 YSDMAANPTYRQOFTQSVDLFQYKFPDGLDWEYPGSLGNPKIKDNYLALVRELKD 185
Db 123 FSAASAAGELAKRFISDCVAFQPHGFDGIDLWEYPAQRDGNPLIDRNHAQLVEHRE 182
Qy 186 APEPHGYLLTAASVPGKDKIDRAYDIKELNKLFDMMVMYTYDHYHGWENFYGHNAPLYKR 245
Db 183 EFDHYGLLLTAASVAFSAGVSDIPRISKSFPLANVMYDMHGAWDSYCGINAPLYRG 242
Qy 246 PDETDLHTYFNVNMTTHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLKGDPAKNSP 305
Db 243 SADTDLRQLQINNVASIFHFWLAQCGTGRKLVGLIPLYGRNFTLASAANTQIGAPTGGGT 302
Qy 306 PGFTSGEGVLSYELCOLFQKEWHIOYDEYNAPYGYNDKIWGVYDDLASISCKLAPL 365
Db 303 VGRYTRPGVMGYNEFEKLEATEADWLNSEQOQVPAVRNNQWVGYYDDLSVQLKVYL 362
Qy 366 KELGVSGVMWSLENDDFKHC-GPKNPLLNKNVNMINGDEKNSFECILGSPSTTPTPT 424
Db 363 LDQGLGAMVWSLETDGFLVCGGGRYPLMHEIRSLVNGGT-----PSTTTMPPSV 413
Qy 425 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPT 484
Db 414 APTT-----STVAPGTTTTPTGANPGTTPPT--SDAPNHTTTTSTTTTGNPGTTRP 466
Qy 485 TTTEHTSETPKYTVTVVGDHLIKCY--KEGDI PHPTNIHKYLVC-----EFVNGGWWH 535
Db 467 -----DG---PCAGRGYGFVPHPTNCARYIICLTADTYYEFT----- 500
Qy 536 IMPCPPPGTIW 545
Db 501 ---CPPGTLP 507

RESULT 5
Q7Q5I7 ANOGA
ID Q7Q5I7 ANOGA PRELIMINARY; PRT; 525 AA.
AC Q7Q5I7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000020485.
GN ORFNames=ENSANGG00000017996;
OS Anopheles gambiae str. PEST.
OC Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB801008960; EAA10725.2; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
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DR GO:0006030; P:chitin metabolism; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR011583; Chitinase II.
DR InterPro: IPR002557; Chitin bind PerA.
DR InterPro: IPR001223; Glyco_hydro_18.
DR InterPro: IPR001579; Glyco_hydro_18AS.
DR Pfam: PF01607; CBM_14; 1.
DR ProDom: PD000471; Chitinase II; 1.
DR SMART: SM00494; ChtBD2; 1.
DR SMART: SM00636; Glyco_18; 1.
DR PROSITE: PS01095; CHITINASE_18; 1.
DR PROSITE: PS0940; CHIT_BIND_II; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 525 AA; 56998 MW; 36B452250257DF1 CRC64;

Query Match 32.4%; Score 1006.5; DB 2; Length 525;
Best Local Similarity 37.1%; Pred. No. 1.5e-48;
Matches 204; Conservative 98; Mismatches 189; Indels 59; Gaps 10;

QY 8 LSINACIGLMNASIKRD--HNDYSKNPMRIVCVGTWTSVYHKVD-PYTTIEDIDPPKCTHLM 65
DB 5 VGVLVLVAFAAEAPHKASAEKKVVCVGTWATYRPGNGRYDIEHDPSLCTHLM 64
QY 66 YGFAKIDYKTYIQVDFPYQDDNHNHNSWEKRGYERFNNLRNLKNPELTMTWISLGGWYEGSEK 125
DB 65 YGFFGINE-DATVRIIDPYLDLEN-WGRGHKRFVGLKNVAPGLKTLAAIGGWNEGSRK 122
QY 126 YSDMAANTYQQFQISQVLDFOEYKFDGLDWEYFGSRNLGNPKIDKQNYLALVRELKD 185
DB 123 FSAAMASGELKRFISDCVAFQCRHGFPGDGLDWEYPAQRDGNPLDIRDNHAQLVEEMRE 182
QY 186 APEPHGYLLTAASVPGDKIDRAYDIKELNKLFDMMNVTYDYGHWENFYGHNAPLYKR 245
DB 193 EFDHYGLLTAASVFSAGSVSDIPIKSFHFLNVMVDMHGANDSYCGINAPLYRG 242
QY 246 PDETDELHTYFNVNVTMHHYLLNNGATRDKLVGVFPFYGRAMSIDRSKLKLGDPKAGMSP 305
DB 243 SADTTDRLGQMVNNAISIQFWLAQGAPEKLVLGIPLYGRSFTLANAANTQIGAPTVGGT 302
QY 306 PGFISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGNKDWYDDDLASISCKLAPL 365
DB 303 AGPYTRFPGVGYNEFECFKLATEAWDLRSEBQQVYAVRNQWGLYDGLRSVLQKVYL 362
QY 366 KELGVSVVMVSLNDDFKGHC-GPKNPLLNKVNHNMGDEKNSPECILGPSTTTPTT 424
DB 363 LDQGLGGANVMSLETDDFLVCGGGRYPLMHEIRSLVNGG----- 402
QY 425 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 484
DB 403 --TPSTTTQPPSVASTTTTTPAGTPTTTTTPGANPGTTQPPPTSDAPNHTTTTSTTGAAPG 459
QY 485 TTTEHTSETPKTYTVVDGHLIKCY--KSGDIPHPNTHIKYLC-----EFVNGWVWV 535
DB 460 TTQPPSGDGP-----CAGGRYGFVHPHTNCARYICLTADTYVEFT----- 500
QY 536 IMPCPPGTIW 545
DB 501 ---CPPGTLF 507

RESULT 6
Q81SH5_9ARAC PRELIMINARY; PRT; 431 AA.
AC Q81SH5_
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Chitinase.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Eucelleginae; Araneolidae; Araneidae; Araneus.
OX NCBI_TaxID=182803;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15694591; DOI=10.1016/j.cbpc.2004.11.009;
RA Han J.H., Lee K.S., Li J., Kim I., Je Y.H., Kim D.H., Sohn H.D.,
RA Jin B.R.;
RT "Cloning and expression of a fat body-specific chitinase cDNA from the
RT spider, Araneus ventricosus.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 140:427-435(2005).
DR EMBL; AY120879; AAN39100.1; -; mRNA.
DR HSSP; Q13231; 1LIG2.
DR GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO:0005975; P:carbohydrate metabolism; IEA.
DR GO:0008152; P:metabolism; IEA.
DR InterPro: IPR011583; Chitinase II.
DR InterPro: IPR001223; Glyco_hydro_18.
DR InterPro: IPR001579; Glyco_hydro_18AS.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR SMART: SM00636; Glyco_18; 1.
DR PROSITE: PS01095; CHITINASE_18; UNKNOWN_1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 431 AA; 47238 MW; 929439397B9BC923 CRC64;

Query Match 30.3%; Score 942; DB 2; Length 431;
Best Local Similarity 43.6%; Pred. No. 5e-45;
Matches 185; Conservative 78; Mismatches 135; Indels 26; Gaps 9;

QY 12 ACIGLM--NASIKRDHNDYSKNPMRIVCVYVGTWTSVYHKVD-PYTTIEDIDPPKCTHLMYGF 68
DB 6 ACLLLLLVAVASAQRDRNQKKYKVCYILGSMANYRGEGKPLIEHIDPFLCTHVIYGF 65
QY 69 AKIDYKTYIQVDFPYQDDNHNHNSWEKRGYERFNNLRNLKNPELTMTWISLGGWYEGSEKYS 128
DB 66 AKLSNNQ--IAYDYPYLDLEN-WGLGAFQRFNNLKKTNPQLSTLIAIGGWNEGSKYSA 122
QY 129 MAANPTYQQFQISQVLDFOEYKFDGLDWEYFGSRNLGNPKIDKQNYLALVRELKDAFE 188
DB 123 MAADPNARATFVKSVIDFCUKYDFDGLDMDWEYPANR--GGAHDKQNFVTLKELKEAFA 181
QY 189 PHGYLLTAASVPGDKIDRAYDIKELNKLFDMMNVTYDYGHWENFYGHNAPLYKRPDE 248
DB 182 PHGILLSAASVAGKNTIDTAYDIPGAKYLDIFINVMAYDLHGSWEKTAGHNAPLYERPGE 241
QY 249 TDELHTYFNVNVTMHHYLLNNGATRDKLVGVFPFYGRAMSIDRSKLKLGDPKAGMSPPGF 308
DB 242 -PESDKILNVDYAINYWKNGTPKNKVLGMGTGYSFTLANAANGLGAATTGPGSAGP 300
QY 309 ISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGNDKIWWGVYDDDLASISCKLAPLKL 368
DB 301 LTKEPGMLGYNEIC---SDKGNVEFVEKVEAPYAKGNQWGVYDSVKSIGIKVDYLIRE 357
QY 369 GVSQVMVMSLENDDFKGHC-GPKNPLLNKVNHNMGDEKNSPECILGPSTTTPTPTPTPT 427
DB 358 GLGGMIWSLETDDFRGCGGKYPPLTTTIAKLNGLD-----VARPTDPK 403
QY 428 TPTT 431
DB 404 QPTT 407

RESULT 7
O17412_AEDAE PRELIMINARY; PRT; 1635 AA.
ID O17412_AEDAE
AC O17412;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Chitinase.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Culicinae; Culicini; Aedes; Stegomyia.
OX NCBI_TaxID=7159;
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DR InterPro; IPR002557; Chitin bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChetB2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS0940; CHIT_BIND_II; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 544 AA; 61069 MW; 89872DFCIDA23753 CRC64;

Query Match 27.3%; Score 847; DB 2; Length 544;
Best Local Similarity 36.5%; Pred. NO. 1.4e-39;
Matches 207; Conservative 78; Mismatches 218; Indels 64; Gaps 19;

Qy 1 M K T I Y A I L S I N A - C I G L M N A S I K D H N D Y S K N P R I I V C V G T W S V Y H K - V D P Y T I E D I D P 58
Db 1 M R A I P A T L A V L A S C A A L V Q C A D S R - - - - - A R I V C Y F S N W A V Y R P G V G R Y G I E D I P V 51
Qy 59 F K C T H L M Y G F A K I D E Y K Y T I Q V F D P Y Q D D N H S M E K R G Y E R F N N L R K N P E L T T M I S L G G 118
Db 52 D L C T H L I Y S F I G V T E K S E V L I I D P E L D - - - - - V D K S G F R N F T S I R S K H P D V K F M V A V G G 106
Qy 119 W Y E G S E K Y S D M A A N P T V R Q Q F I Q S V L D F L Q Y K F D G L D L D W E Y P G S R - L G N P K I D K Q N Y L 177
Db 107 W A E G S K Y S H M V A Q K S T M S I R S V D F L K K Y D F D G L D L D W E Y P G A A D R G S G S F S D K D E F L 166
Qy 178 A L V P E L K D A F - E P H G Y L L T A A V S P G K I D R A V D I K E L N K L F D M N V M T Y D H G W E N F 235
Db 167 Y F V Q E L K R A F I R A D R G W E L T A A V L A N P R L M E G H V P E L C Q E L D A I H V M S Y D L R N W A G F 226
Qy 236 Y G H N A P L Y K R D E T D E L H T Y F N V N Y T H Y I L N G A T R D K L V M G V P F Y G R A M S I E D - - - - - 290
Db 227 A D V H S P L Y K R P H D - Q W A Y E K L N V N D G L N W E E K G C P T N K L V G P F Y G R S F T L S A G N N Y 285
Qy 291 - - - - - R S K J L K G D A Q M S P P G F T S G E G V L S Y I E L C Q L F Q K E - - E W H I Y D E Y N A P Y 342
Db 286 G L G T Y I N K E A G G D P A P Y N A T G F - - - - - W A Y Y E I C T E V D A D G S G W T K W D B F G K C P Y 338
Qy 343 G Y N D K I W G Y D D L A S I C K L A F L E L G V G W V M S L E N D D P K G C G P N P L N K V H N M I N 402
Db 339 A Y K G T Q W G Y E D P R S V E I R M N W I K E G Y L G A M T W A I D M D D F K L G L G E E N P L I K L H L - - - - - 394
Qy 403 G D E K N S F P C I L G P S T T - - - T P T P T T P T T P T T P T T P T T P T T P T T P T T P T T P T T P T T P 459
Db 395 - - - K H M S Y T V P P A R T G H A T P P E W - - A R P S T P S D P S E G D P I - - - - - P T T T T T V K P T T 445
Qy 460 T T T P S P T T P T T P T P A P T T P S P T T T E H S E T P K Y T Y V D G H L I K Y K E G D - I P H P T N 518
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Qy 519 I H K Y L V C F V N G G W V W H M P C P G T I W 545
Db 503 C S K Y W R C - - V N G E G V Q - - F S C Q P G T I F 525

RESULT 12
QW2M7 DROME
ID QW2M7 DROME PRELIMINARY; PRT; 476 AA.
AC QW2M7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE CG9357-PA.
GN Name=CG9357; ORFNames=CG9357;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.

MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Bolthakos S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
NUCLEOTIDE SEQUENCE.
MEDLINE=12537568; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomes perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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QY 261 TMHYLLNNGATRDKLVMGVFFYGRAWSIEDRSKLLKGDPAKMGSPPGFISGEEGVLSYIE 320
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QY 380 NDDFKGHCG-PKNPLLNKVNHNMGDEKNSFECILGPSTTPT--PTTTPT--TTTTPT- 434
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DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Chitinase precursor (EC 3.2.1.14).
GN Name=chiB4;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
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RC STRAIN=Kinsu x Showa; TISSUE=integument;
RX MEDLINE=22172809; PubMed=12045191; DOI=10.1074/jbc.M112422200;
RA Abdel-Banat B.M.A.; Koga D.;
RT "Alternative splicing of the primary transcript generates
RT heterogeneity within the products of the gene for Bombyx mori
RT chitinase."
RL J. Biol. Chem. 277:30524-30534 (2002).
DR EMBL; AF455139; AAL51080.1; -; mRNA.
DR HSP; Q13231.1LG2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR011583; Chitinase II.
DR InterPro; IPR002557; Chitin bind PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBW_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00940; CHIT_BIND_II; 1.
KW Glycosidase; Hydrolase; Signal.
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FT CHAIN 22 566 chitinase.
SQ SEQUENCE 566 AA; 63465 MW; 43FC717B3F6917D0 CRC64;

Query Match 27.0%; Score 839; DB 2; Length 566;
Best Local Similarity 35.9%; Pred. No. 4.1e-39;
Matches 207; Conservative 78; Mismatches 209; Indels 82; Gaps 20;

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Db 1 MRAIFATLAVLASCAALVQCADSR-----ARIVCFSNWAVYRPGVGRYGIETIPV 51
QY 59 FKTHLMYGAIDYKYTIQVDPYQDDNHNSEKGYERFNNLRILKNPELTTMISLGG 118
Db 52 DLCTHLIYSIGVTEKSEVLIIIDPELD-----VDKSGFRNFTSLRSGKHPDVKFMVAVGG 106
QY 119 WYEGSEKYSMAANPTYRQOFIQSVLPLOEYKFDGLDWEYPGSR-LGNPKIDKKNYL 177
Db 107 WAEGGKYSIMVAQKSTRMSFIRSVDFLKKYDFDGLDWEYFGAADRGSGFSKDKFL 166
QY 178 ALVRELKDAF--EPHGYLLTAASVPGKDKIDRAYDIKELNKLFDMMNMVMTYDHHGWNF 235
Db 167 YFVQELKRAFIRAGRGWELTAAPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGF 226
QY 236 YGNAPLYKRPDETDELHTYFNVNYTHYVLLNNGATRDKLVMGVFPYGRAWSIED----- 290
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QY 291 -----RSKLKGDPAKMGSPPGFISGEEGVLSYIELCOLFOKE--BWHIQYDEYYNAPY 342
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QY 343 GYNDKIWGYDLDASISCKLAPLKLKELGVGVMMVWLENDDPKHGCGKPNLLNKVHNMIN 402
Db 339 AYKGTQWGVYEDPRSVEIKMNWIKKGYLGAWTWAIDMDDFKGLCGEENPLIKLLHKHMS 398
QY 403 GDEKNSFECILGPSTTPTTPTTPTTPTTPTTPTTPTT-----TPSPPTTPTTPTT 458
Db 399 -----TYTVPPARTGHTTPTPEWARP-PSTPSDPSSEGDPIPTTTTIVKPTT 444
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AC P36362;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endochitinase precursor (EC 3.2.1.14).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93357793; PubMed=8353525; DOI=10.1016/0965-1748(93)90043-R;
RA Kramer K.J.; Corpuz L.; Choi H.K.; Muthukrishnan S.;
RT "Sequence of a cDNA and expression of the gene encoding epidermal and
RT gut chitinases of Manduca sexta.";
RL Insect Biochem. Mol. Biol. 23:691-701 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97215580; PubMed=9061927; DOI=10.1016/S0965-1748(96)00066-5;
RA Choi H.K.; Choi K.H.; Kramer K.J.; Muthukrishnan S.;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:19:31 ; Search time 169 Seconds
(without alignments)
1372.161 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3107	100.0	555	4	US-10-218-743-18
3	3014	97.0	536	4	US-10-218-743-21
4	2542	81.8	509	4	US-10-218-743-35
5	2542	81.8	509	4	US-10-218-743-38
6	2475	79.7	490	4	US-10-218-743-41
7	854.5	27.5	4498	4	US-10-712-124-68
8	854.5	27.5	4498	6	US-11-097-143-2577
9	837.5	27.0	4595	6	US-11-097-143-42003
10	832	26.8	460	6	US-11-097-143-19890
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12	738	23.8	445	5	US-10-787-845-10
13	738	23.8	466	2	US-08-663-618A-2
14	738	23.8	466	3	US-09-977-827-4
15	738	23.8	466	4	US-10-161-547-2
16	738	23.8	466	5	US-10-723-860-1352
17	738	23.8	466	5	US-10-756-149-5051
18	738	23.8	466	6	US-11-063-574A-16
19	737.5	23.7	520	4	US-10-268-913-3
20	736.5	23.7	473	4	US-10-004-219B-4
21	736.5	23.7	473	5	US-10-787-845-4
22	735.5	23.7	459	4	US-10-382-248-38
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39	708.5	22.8	455	5	US-10-787-845-14	Sequence 14, Appli
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ALIGNMENTS

RESULT 1

US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match	100.0%	Score 3107;	DB 4;	Length 555;
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301 KGMSPPGFISGEEGVLSEIQLCOLFOKEBWHIQYDEYNAPYGYNDKIWVGVDLASC 360
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RESULT 2

US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-18

Query Match 100.0%; Score 3107; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIIVAILSIMACIGLMMASIKRDNDYSKNPMRIVCVYGTWSVYHKVDPTYIEDIDPFK 60
DB |||||
1 MKTIIVAILSIMACIGLMMASIKRDNDYSKNPMRIVCVYGTWSVYHKVDPTYIEDIDPFK 60
QY 61 CTHLMYGAKEIDYKYYTQVDFPYQDDNHNNSWEKRGYERFNNLRKLNPELTMTISLGGWY 120
DB |||||
61 CTHLMYGAKEIDYKYYTQVDFPYQDDNHNNSWEKRGYERFNNLRKLNPELTMTISLGGWY 120
QY 121 EGSEKYSMAANPTTYRQFIQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALV 180
DB |||||
121 EGSEKYSMAANPTTYRQFIQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALV 180

QY 181 RELKDAPEPHGYLLTAAVSPGOKIDRAYDIKELNKLFDWMNVMTYDHYHGWNFYGHNA 240
DB |||||
181 RELKDAPEPHGYLLTAAVSPGOKIDRAYDIKELNKLFDWMNVMTYDHYHGWNFYGHNA 240
QY 241 PLYKRPDETDLHTYFNVNNTMHHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
DB |||||
241 PLYKRPDETDLHTYFNVNNTMHHYLLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPDA 300
QY 301 KGMSPPGFISGEEGVLSEIQLCOLFOKEBWHIQYDEYNAPYGYNDKIWVGVDLASC 360
DB |||||
301 KGMSPPGFISGEEGVLSEIQLCOLFOKEBWHIQYDEYNAPYGYNDKIWVGVDLASC 360
QY 361 KLAFLKELGVSGVMVMSLENDDFKGHCQPKNPLLNKNVNMINGDEKNSFECILGSPSTTP 420
DB |||||
361 KLAFLKELGVSGVMVMSLENDDFKGHCQPKNPLLNKNVNMINGDEKNSFECILGSPSTTP 420
QY 421 TPPT 480
DB |||||
421 TPPT 480
QY 481 TPSPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCP 540
DB |||||
481 TPSPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCP 540
QY 541 PGTIWCQEKLTICGE 555
DB |||||
541 PGTIWCQEKLTICGE 555

RESULT 3

US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-21

Query Match 97.0%; Score 3014; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.7e-195;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 SIKRDNDYSKNPMRIVCVYGTWSVYHKVDPTYIEDIDPFKCTHLMYGAKEIDYKYYTQ 79
DB |||||
1 SIKRDNDYSKNPMRIVCVYGTWSVYHKVDPTYIEDIDPFKCTHLMYGAKEIDYKYYTQ 60
QY 80 VFDPYQDDNHNNSWEKRGYERFNNLRKLNPELTMTISLGGWYEGSEKYSMAANPTTYRQOF 139
DB |||||
61 VFDPYQDDNHNNSWEKRGYERFNNLRKLNPELTMTISLGGWYEGSEKYSMAANPTTYRQOF 120
QY 140 IQSVLDFLOEYKFDGLDLDWEYPGSLGNPKIDKQNYLALVRELKDAPEPHGYLLTAAVS 199

Db 121 IQSVLDFLQEKYKFDGLDLDWEYPSGRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAS 180
QY 200 PGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYCHNAPLYKRPDETDELHTYFNN 259
Db 181 PGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYCHNAPLYKRPDETDELHTYFNN 240
QY 260 YTHYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPKAGMSPPGFISGEGVLSYI 319
Db 241 YTHYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPKAGMSPPGFISGEGVLSYI 300
QY 320 ELCQLFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGSGVNMVWSLE 379
Db 301 ELCQLFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISCKLAFKELGSGVNMVWSLE 360
QY 380 NDDFKGHCPCPKPLKVNHNMININGDEKNSFECILGPSTPTPTPTPTPTPTPTPTPTPT 439
Db 361 NDDFKGHCPCPKPLKVNHNMININGDEKNSFECILGPSTPTPTPTPTPTPTPTPTPTPT 420
QY 440 TPTTPT 499
Db 421 TPTTPT 480
QY 500 VDGLHIKCYKEGDIHPHTNIHKYLVCEPVNGGWWVHIMPCPPGTTWCQKLTICGE 555
Db 481 VDGLHIKCYKEGDIHPHTNIHKYLVCEPVNGGWWVHIMPCPPGTTWCQKLTICGE 536

RESULT 4

US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35

Query Match 81.8%; Score 2542; DB 4; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.4e-163;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLNNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTIEDIDPFK 60
Db 1 MKTTFALFCIWACIGLNNAAATKRDHNNYSKNPMRIVCVGTWSVYHKVDPTIEDIDPFK 60
QY 61 CTHLMYGFPAKIDYKYTIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
Db 61 CTHLMYGFPAKIDYKYTIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
QY 121 EGSEKYSMAANPTYROQFVQSVLDFLQEKYKFDGLDLDWEYPSGRLGNPKIDKQNYLALV 180

Db 121 EGSEKYSMAANPTYROQFVQSVLDFLQEKYKFDGLDLDWEYPSGRLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAASVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYCHNA 240
Db 181 RELKDAFEPHGYLLTAASVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYCHNA 240
QY 241 PLYKRPDETDELHTYFNNVNTMYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPGA 300
Db 241 PLYKRPDETDELHTYFNNVNTMYLLNNGATRDKLVMGVPPYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPGFISGEGVLSYIELCOLFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISCK 360
Db 301 KGMSPGFITGEEGVLVSYIELCOLFQKEWHIQYDEYNNAPYGYNDKIWGYDDLASISCK 360
QY 361 KLAFLKELGSGVNMVWSLENDDFKGCPCPKPLKVNHNMININGDEKNSFECILGPSTPTPT 420
Db 361 KLAFLKELGSGVNMVWSLENDDFKGCPCPKPLKVNHNMININGDEKNSFECILGPSTPTPT 420
QY 421 TPTTPT 480
Db 421 TPTTPT 434
QY 481 TPTTPT 537
Db 435 ---PTTDDTSETPKYTYIDGHLIKCYKQGYLPHTDVKYLVCEYIATPNSGWWVHIM 491
QY 538 PCPPTWCQKLTICGE 555
Db 492 DCPKGTWRHATLKNKCIQE 509

RESULT 5

US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-38

Query Match 81.8%; Score 2542; DB 4; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.4e-163;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;
QY 1 MKTIYAILSIMACIGLNNASIKRDHNDYSKNPMRIVCVGTWSVYHKVDPTIEDIDPFK 60
Db 1 MKTTFALFCIWACIGLNNAAATKRDHNNYSKNPMRIVCVGTWSVYHKVDPTIEDIDPFK 60
QY 61 CTHLMYGFPAKIDYKYTIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120
Db 61 CTHLMYGFPAKIDYKYTIQVDFPDYQDDNHNHNSWEKRGYERFNNLRKNPELTMTISLGWY 120


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QY 29 SKNPMRIYCVGTWSYTHK-VDPYTIEDIDPKFCHLMYGFADIKYKTYQVFPYQDD 87
Db 23 SDQASRIYCVFENWAVYRTIGRYGLEDPADLCTHIIYVTFGVNDKSDWLVLDPELD- 81
QY 88 NHNSKEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSMDAANPTVROQFIQSVLDFL 147
Db 82 ----VDQGGFSKFTQLKSNPNVLEIAVGGWAGGSKYSQWAVVDRRQSRFIRSVVRFM 137
QY 148 QBYKFDGLDWEYEGS--RLGNPKIDKQNYLALVRELKDAF--BPHGYLLTAAVSPGKD 203
Db 138 KOYNFDGFDLWEYFGATDRGNYG-DKDKFLYFVEELRAFDGRGRGWEITMAVPVAKF 196
QY 204 KIDRAYDIKELNKLFDMMNVMYDYHGGWENFYGHNAPLYKRPDSTDELHTYFVNYNVTMH 263
Db 197 RLNEGYPHELCEALDAHAMTYDLRGNWAGPADVHSPLYKXKHD-QVAYEKLNVNDGLA 255
QY 264 YLLNNGATRDKLVMGVFPFGRAWSIEDRSK-LKLG---DPAKGMSPRGFISGEEGVLSYI 319
Db 256 LMEEMGCPANKLVGVFPFYGRFTTILSNKNKNMGTIYNKEAGGAGPGYTNASGLLAYI 315
QY 320 ELC-QLFOKEE-WHIOYDEYNAPYGYNDKIWVGYYDDLASISCKLAFKLKELGVSVMVWS 377
Db 316 ELCTEVMDSKWTWEDDAGVPTYKDTQWGVYENASIQIKWDFIKQRYAGATWA 375
QY 378 LENDDFKHGCGKPNLLNKHV-NMINGDEKNSFECILGSPSTTPTTTP-----TPTTTT 432
Db 376 IDMDDFHGCGRKNGLTQILYDNMKN-----YRVPEPTRQTTPEWAKPPAT 423
QY 433 PTPP-----SPTTPT-----TPSPPTPTTPS---PTTPTTPTTPTTPTTP-- 473
Db 424 PNPDEGAVAPTSTTKRKPCKPXTSPLSPTSAQGVPTVGSSTPKPTTKPKPKPKPK 483
QY 474 TPAPTTPSPPTTTHSTPKYTY-----VDGHLIKYKCGEDIDHP 516
Db 484 TTTTTTTPAP---EKSTEPESEVYVVDVPEPTDPEQPMGQFDPNEIDCTNDFVHP 540
QY 517 TNIHKYLVEFVNGWVHIMP-----CPPGT 543
Db 541 -NCRKYFR-----VHGKPVPECKEGT 562
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RESULT 10

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US-11-097-143-19890
; Sequence 19890, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 19890
; LENGTH: 460
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19890

Query Match 26.8%, Score 832; DB 6; Length 460;
Best Local Similarity 33.7%; Pred. No. 6.1e-48;
Matches 183; Conservative 87; Mismatches 175; Indels 98; Gaps 11;

QY 17 MNASIKRDNDYSKNPMRIYCVGTWSYTHK-VDPYTIEDIDPKFCHLMYGFADIKYK 75
Db 1 MAASSSAQNGS-SKN---VVCYQGTWSVYRPGKFGMEDIDPFLCTHIIYAFAGIEB-T 55
QY 76 YTIQVFPYQDDNHNHNSWEKGYERFNNLRKLNPELTTMISLGGWYEGSEKYSMDAANPTY 135
Db 56 QGLAVIDAYDLDEENS-GRGNIKSFNALKLNPNVLTVAVGGWNEGSKRESLVARDPDSK 114
QY 136 RQFIQSVLDFLQBYKFDGLDWEYFGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLT 195
Db 115 REKFVDDVVRFLQRFHGFGLDWEYFQGRHSLDNEEDRSNYITFLKELKEGLEPFGFTLS 174
QY 196 AAVSPGDKIDRAYDIKELNKLFDMMNVMYDYHGGWENFYGHNAPLY---KRPDETDEL 252
Db 175 AAVSAGSABEISIDIFAMVPYLDLIINMAYDLHGPDQVVGINAPLYAAEKDASDSSGR 234
QY 253 HTYFNVNVTMHHYLLNNGATRDKLVMGVFPFYGRAWSIEDRSKLGDPAGKMSPPGFISGE 312
Db 235 QQQLNDAVDAVVKYLKAGAPAEKILGVFPFYGRSFTLATAEGNQPGAPHIGKIAGNYSRE 294
QY 313 EGVLSYIELCOLFOKEBWHIOYDEYNAPYGYNDKIWVGYYDDLASISCKLAFKLKELGVSG 372
Db 295 PGVLGYNELCMBEREEMTKWEATQVYAYRQRWGVYEDPRSLKALKQAYVMDNHLGG 354
QY 373 VMVWSLENDDFKHGCGPK-NPLLKNKHVNMINGDEKNSFECILGSPSTTPTTPTTPTTPTT 431
Db 355 IMIWSLGSDDFRGTCGGQPYPLLHEINRVLFGG----- 387
QY 432 TPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 491
Db 388 -----NTPSGLTTESNR 399
QY 492 ETPK--YTTYVDGHLIKYKCGEDIPHTNIHKYLVCBFGWGVVHIMPCTPGTIWCOEK 549
Db 400 ESPSEGFSCPAD-----PAGYIRDPDNCCKFYC-----SGGKTHNFDPCPSGLNFDLDT 449
QY 550 LTC 552
Db 450 KSC 452

RESULT 11
US-10-004-219B-10
; Sequence 10, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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LOCATION: (1)..(445)
OTHER INFORMATION: /note="Human chitotriosidase"
US-10-004-2198-10

Query Match 23.8%; Score 738; DB 4; Length 445;
Best Local Similarity 34.2%; Pred. No. 1.3e-41;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

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QY 34 RIVCVGTWSVVKVDP-YTIEDIPPKCTHLMVGFADKIDVYKIQVDFPDYQDDNNHNSW 92
DB 2 KLVCFYTNWAQYRQGEARFLPKDLPCLTHLIYAFAGTNHQLST-----TSM 50

QY 93 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSIDMAANTYRQOFTQSVLDLQYK 151
DB 51 NDETLVQBFNGLKKNPKLKTLLAIGGNWFGTKFTDMVATANNRQTTFVNSAIRFLRKY 110

QY 152 FDGLDLDWEYPSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAASPGDKK 204
DB 111 FDGLDLDWEYPSGQ-GSPAVDKERFTLLVQDLANAFQQAOTSGKERLILLSSAAVPAQOTY 169

QY 205 IDRAVDIKELNKLFDMMVMVTYDYGWENFYGHNAPLYKRPDETDLHTYFNVNVTMHY 264
DB 170 VDAGEVDKIAQNLDVNLMAVDYFGSWKVTGHSNPLYKQESGAAAS-LNVDAAVQO 228

QY 265 YLNNGATRDKLVGMVFPFYGRAWSIEDRSKLGDDPAKMSPPGFTSGEGVLSYIELCOL 324
DB 229 WLQKTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPTKEGMLAYVEVCSW 288

QY 325 FQKEWHIOYDEYNNAPYGNDKIWKGYDDLASISCKLAFKELVSGVMMWSLENDDPK 384
DB 289 KGATKQRIQ-DO--KVPYIFRDNQWVGPDVSEFKTKVSYLKQKGLGGAMWALDLDFA 345

QY 385 GHCGPKNLLKNVHNMINGDEKNSPECILGPSTTTPTTTPTTTPTTTPTTTPTTTPTTT 444
DB 346 G-----FSCNQ-----RYPLIQTLRQELSLPYLPST 373

QY 445 PSPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 469
DB 374 PELEVP-KPGQPSPEHGHSPGQDT 397
```

RESULT 12

US-10-787-845-10
Sequence 10, Application US/10787845
Publication No. US20040253224A1

GENERAL INFORMATION:
APPLICANT: Macrozyme
APPLICANT: Aerts, Johannes M.F.G.
APPLICANT: Boot, Rolf G.
TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
FILE REFERENCE: 2183-5136US
CURRENT APPLICATION NUMBER: US/10/787,845
PRIOR FILING DATE: 2004-02-26
PRIOR FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(445)
OTHER INFORMATION: /note="Human chitotriosidase"
US-10-787-845-10

Query Match 23.8%; Score 738; DB 5; Length 445;
Best Local Similarity 34.2%; Pred. No. 1.3e-41;
Matches 152; Conservative 85; Mismatches 150; Indels 59; Gaps 11;

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QY 34 RIVCVGTWSVVKVDP-YTIEDIPPKCTHLMVGFADKIDVYKIQVDFPDYQDDNNHNSW 92
DB 2 KLVCFYTNWAQYRQGEARFLPKDLPCLTHLIYAFAGTNHQLST-----TSM 50

QY 93 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSIDMAANTYRQOFTQSVLDLQYK 151
DB 51 NDETLVQBFNGLKKNPKLKTLLAIGGNWFGTKFTDMVATANNRQTTFVNSAIRFLRKY 110

QY 152 FDGLDLDWEYPSRGLGNPKIDKQNYLALVRELKDAPEPHG-----YLLTAASPGDKK 204
DB 111 FDGLDLDWEYPSGQ-GSPAVDKERFTLLVQDLANAFQQAOTSGKERLILLSSAAVPAQOTY 169

QY 205 IDRAVDIKELNKLFDMMVMVTYDYGWENFYGHNAPLYKRPDETDLHTYFNVNVTMHY 264
DB 170 VDAGEVDKIAQNLDVNLMAVDYFGSWKVTGHSNPLYKQESGAAAS-LNVDAAVQO 228

QY 265 YLNNGATRDKLVGMVFPFYGRAWSIEDRSKLGDDPAKMSPPGFTSGEGVLSYIELCOL 324
DB 229 WLQKTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPTKEGMLAYVEVCSW 288

QY 325 FQKEWHIOYDEYNNAPYGNDKIWKGYDDLASISCKLAFKELVSGVMMWSLENDDPK 384
DB 289 KGATKQRIQ-DO--KVPYIFRDNQWVGPDVSEFKTKVSYLKQKGLGGAMWALDLDFA 345

QY 385 GHCGPKNLLKNVHNMINGDEKNSPECILGPSTTTPTTTPTTTPTTTPTTTPTTTPTTT 444
DB 346 G-----FSCNQ-----RYPLIQTLRQELSLPYLPST 373

QY 445 PSPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 469
DB 374 PELEVP-KPGQPSPEHGHSPGQDT 397
```

RESULT 13

US-08-663-618A-2
Sequence 2, Application US/08663618A
Publication No. US20030017570A1

GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Chitinase Materials and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,618A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/32960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-663-618A-2

```
Query Match 23.8%; Score 738; DB 2; Length 466;
Best Local Similarity 34.2%; Pred. No. 1.4e-41;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 34 RIVCVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFPAKIDYKTIQVDFPDYQDDNHNWS 92
DB 23 KLVCFYTNWAQYRQGEARFLPKDLPDLPSLCTHLIYAFAGMTHQLST-----TEW 71

QY 93 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSDMAANTYRQQTQSVDLFQBYK 151
DB 72 NDETLYQEFNGLKKNPKLKTLLAIGGNWFGTKFTDMVATANNRQTFVNSAIRFLRKY 131

QY 152 FDGLDLDWEYPSGRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASPGKDK 204
DB 132 FDGLDLDWEYPSGQ-GSPAVDKERFTTLVQDLANAFQQAQTSKGERLLLSAAVPAQGT 190

QY 205 IDRAVDIKELNKLFDMMNVTYDHGGWENFYGHNAPLYKRDETDLHTYFNNVYTHY 264
DB 191 VDAGYEVDKIAQNLDVNLMAIDFHGSWEKVTGHSPLYKQESGAAAS-LNVDAAVQQ 249

QY 265 YLNNGATRDKLVGMGVPFYGRAWSIEDRSKLGDPAPKMGSPPGFISGEGVLSYIELCOL 324
DB 250 WLQKGTTPASKLILGMPTYGRSFTLLASSSDTRVGAPATGSGTGPPTKEGMLAYYEVCSW 309

QY 325 FQKEWHIOYDEYNNAPYNDKIWGYDDLASISCKLAFKELGVSGVMWWSLENDPFK 384
DB 310 KGATKQRIQ-DQ--KVPIYFRDNQWVGDFDVSFRTKVSYLKQKGLGAMWVALDLDFA 366

QY 385 GHCGPKNPLLNKVNHNMGDEKNSFECILGPSTTPTPTPTPTPTPTPTPTPTPTPT 444
DB 367 G-----FSCNQ-----RYPLIQTLRQELSLPYLPST 394

QY 445 PSPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 469
DB 395 PELEVP-KPGQSPSEPHGSPGQDT 418

RESULT 15
US-10-161-547-2
; Sequence 2, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
; FILE REFERENCE: 27866/35407
; CURRENT APPLICATION NUMBER: US/10/161,547
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/267,574
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-547-2

Query Match 23.8%; Score 738; DB 4; Length 466;
Best Local Similarity 34.2%; Pred. No. 1.4e-41;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 34 RIVCVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFPAKIDYKTIQVDFPDYQDDNHNWS 92
DB 23 KLVCFYTNWAQYRQGEARFLPKDLPDLPSLCTHLIYAFAGMTHQLST-----TEW 71

QY 93 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSDMAANTYRQQTQSVDLFQBYK 151
DB 72 NDETLYQEFNGLKKNPKLKTLLAIGGNWFGTKFTDMVATANNRQTFVNSAIRFLRKY 131

QY 152 FDGLDLDWEYPSGRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASPGKDK 204
DB 132 FDGLDLDWEYPSGQ-GSPAVDKERFTTLVQDLANAFQQAQTSKGERLLLSAAVPAQGT 190

QY 205 IDRAVDIKELNKLFDMMNVTYDHGGWENFYGHNAPLYKRDETDLHTYFNNVYTHY 264
DB 191 VDAGYEVDKIAQNLDVNLMAIDFHGSWEKVTGHSPLYKQESGAAAS-LNVDAAVQQ 249

QY 265 YLNNGATRDKLVGMGVPFYGRAWSIEDRSKLGDPAPKMGSPPGFISGEGVLSYIELCOL 324
DB 250 WLQKGTTPASKLILGMPTYGRSFTLLASSSDTRVGAPATGSGTGPPTKEGMLAYYEVCSW 309

QY 325 FQKEWHIOYDEYNNAPYNDKIWGYDDLASISCKLAFKELGVSGVMWWSLENDPFK 384
DB 310 KGATKQRIQ-DQ--KVPIYFRDNQWVGDFDVSFRTKVSYLKQKGLGAMWVALDLDFA 366

QY 385 GHCGPKNPLLNKVNHNMGDEKNSFECILGPSTTPTPTPTPTPTPTPTPTPTPTPT 444
DB 367 G-----FSCNQ-----RYPLIQTLRQELSLPYLPST 394

QY 445 PSPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 469
DB 395 PELEVP-KPGQSPSEPHGSPGQDT 418

RESULT 14
US-09-977-827-4
; Sequence 4, Application US/09977827
; Publication No. US20020086008A1
; GENERAL INFORMATION:
; APPLICANT: Aerts, Johannes Maria F.G.
; TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomp
; TITLE OF INVENTION: chitin, its use in therapy or prophylaxis against infectious dis
; FILE REFERENCE: Docket 294-32 DIVII/CON
; CURRENT APPLICATION NUMBER: US/09/977,827
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-827-4

Query Match 23.8%; Score 738; DB 3; Length 466;
Best Local Similarity 34.2%; Pred. No. 1.4e-41;
Matches 152; Conservative 85; Mismatches 150; Indels 58; Gaps 11;

QY 34 RIVCVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFPAKIDYKTIQVDFPDYQDDNHNWS 92
DB 23 KLVCFYTNWAQYRQGEARFLPKDLPDLPSLCTHLIYAFAGMTHQLST-----TEW 71

QY 93 -EKRGYERFNNLRKNPELTMTISLGGWYEGSEKYSDMAANTYRQQTQSVDLFQBYK 151
DB 72 NDETLYQEFNGLKKNPKLKTLLAIGGNWFGTKFTDMVATANNRQTFVNSAIRFLRKY 131

QY 152 FDGLDLDWEYPSGRLGNPKIDKQNYLALVRELKDAFEPHG-----YLLTAASPGKDK 204
DB 132 FDGLDLDWEYPSGQ-GSPAVDKERFTTLVQDLANAFQQAQTSKGERLLLSAAVPAQGT 190

QY 205 IDRAVDIKELNKLFDMMNVTYDHGGWENFYGHNAPLYKRDETDLHTYFNNVYTHY 264
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Db 367 G-----PSCNQ-----RYPLIOTLRQELSLPYLPSGT 394
Qy 445 PSFTTPTTTPSPPTTPTTTPSPPTTPT 469
Db 395 PELEVP-KFGQSEPEHGFSPGQDT 418

Search completed: March 31, 2006, 15:23:09
Job time : 171 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:20:29 ; Search time 24 Seconds
(without alignments)
703.969 Million cell updates/sec

Title: US-09-662-293-15

Perfect score: 3107

Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPGTIWCQKLTICGE 555

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.New:*

- 1: /SID55/ptodata/2/pubppaa/US08_NEW_PUB pep.*
- 2: /SID55/ptodata/2/pubppaa/US06_NEW_PUB pep.*
- 3: /SID55/ptodata/2/pubppaa/US07_NEW_PUB pep.*
- 4: /SID55/ptodata/2/pubppaa/US09_NEW_PUB pep.*
- 5: /SID55/ptodata/2/pubppaa/US09_NEW_PUB pep.*
- 6: /SID55/ptodata/2/pubppaa/US10_NEW_PUB pep.*
- 7: /SID55/ptodata/2/pubppaa/US11_NEW_PUB pep.*
- 8: /SID55/ptodata/2/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534.5	17.2	595	6	US-10-510-386-240
2	259	8.3	5179	7	US-11-108-172-1068
3	216.5	7.0	548	7	US-11-052-554A-324
4	204	6.6	941	7	US-11-169-232-14
5	204	6.6	1022	7	US-11-169-232-84
6	204	6.6	1038	7	US-11-169-232-74
7	204	6.6	1049	7	US-11-169-232-58
8	204	6.6	1140	7	US-11-169-232-104
9	204	6.6	1270	7	US-11-169-232-44
10	204	6.6	1311	7	US-11-169-232-42
11	204	6.6	1313	7	US-11-169-232-142
12	204	6.6	1314	7	US-11-169-232-50
13	204	6.6	1320	7	US-11-169-232-46
14	204	6.6	1320	7	US-11-169-232-60
15	204	6.6	1334	7	US-11-169-232-48
16	204	6.6	1361	7	US-11-169-232-40
17	204	6.6	1363	7	US-11-169-232-52
18	204	6.6	1404	7	US-11-169-232-2
19	204	6.6	1404	7	US-11-169-232-62
20	191.5	6.2	681	7	US-11-096-568A-2501
21	191.5	6.2	694	7	US-11-096-568A-29818
22	191.5	6.2	717	7	US-11-096-568A-28799
23	190.5	6.1	1970	6	US-10-821-234-1641
24	188	6.1	2011	7	US-11-080-991-56
25	177.5	5.7	364	7	US-11-087-177-31

ALIGNMENTS

RESULT 1

US-10-510-386-240
; Sequence 240, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Ejarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 240
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-240

Query Match		17.2%	Score 534.5;	DB 6;	Length 595;
Best Local Similarity		27.5%	Pred. No. 2.3e-30;		
Matches 169;		Conservative 89;	Mismatches 200;	Indels 157;	Gaps 29;
QY	7	ILSIACIGLMNASIKRDHNDYSKPMRIVCVTWSVTHKVDPTIEDIDPPKCTHLMY	66		
DB	15	IFVWMLSLSFVNGEVAK--ADSGKN-YKIIGYPSMGAYGR--DFQVWMDVSKVGHNY	69		
QY	67	GFAK-----IDSKYTIQVDFDPYQDDNHS-----WEX	94		
DB	70	AFADICWGRHGNPDPTGPNPOTWSCQDENGVIDAPNGTIVMGDPDWDAQKNGPDVWDE	129		
QY	95	--RG-YERFNNRLKNPELTMTISLGGWYEGSEKYSMAANPTYRQOFTQSLVDLPLOEYK	151		
DB	130	PIRGNFKQLLKLSKSHPLKTFISVGGW-TWNRFSVDAADPAARENFAASAVEFLRKYG	188		
QY	152	FGGLDLDWEYP--GRLGN---PKTDKNYLALVRELK-----DAFPHGYLLTAAVSP	200		
DB	189	FDGVLDWEYFVSGGLPGNSTRPE-DKRNYYTLLOEVRKLDAAEAKQKEYLLTTASGA	247		
QY	201	GKDKIDRAVDIKELNKLFDMMNMYDYHGGWENFYGHNAPLYKRPDET-----ELHTYF	256		
DB	248	SPDYVSNT-ELDKIAQTVDWINIMTYDFNGWQSTSAHNAFLYDPKAKEAGVPAETV-	305		
QY	257	NVNYTWHTYLLNNGATRDKLVMGVFPFYGRAWSTEDRSKLGLGDPKAGMSPPGF-----	308		

Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-169-232-14

Query Match 6.6%; Score 204; DB 7; Length 941;
Best Local Similarity 41.8%; Pred. No. 9.8e-07;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LGSPTT-TPTPTT-----PPTP-----TTTTTTPSPTTP-----TTTTTPTTPTT--TPSPT 457
Db 534 LAPTTTKEPTSTSDKPAPTPKGTAPTPKPAPTTPKPAPTPKGTAPTTLKEPAPT 593
QY 458 T-----PTTT-----PSTPTTPTTPT-----PAPTT-STPSPTTTEHTSE 492
Db 594 TPKPAPKELAPTTTGTSTSDKPAPTPKGTAPTPKPAPTTPKPAPTTPKPAPT-----TPE 649
QY 493 TPKYTVYDGHILKCYKSGDIP-----HPTNIHK 521
Db 650 TTPPTT-----SEVSTPTTTKEPTTIHK 672

RESULT 5
US-11-169-232-84
; Sequence 84, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth

Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-11-169-232-84

Query Match 6.6%; Score 204; DB 7; Length 1022;
Best Local Similarity 41.8%; Pred. No. 1.1e-06;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LGSPTT-TPTPTT-----PPTP-----TTTTTTPSPTTP-----TTTTTPTTPTT--TPSPT 457
Db 615 LAPTTTKEPTSTSDKPAPTPKGTAPTPKPAPTTPKPAPTPKGTAPTTLKEPAPT 674
QY 458 T-----PTTT-----PSTPTTPTTPT-----PAPTT-STPSPTTTEHTSE 492
Db 675 TPKPAPKELAPTTTGTSTSDKPAPTPKGTAPTPKPAPTTPKPAPTTPKPAPT-----TPE 730
QY 493 TPKYTVYDGHILKCYKSGDIP-----HPTNIHK 521
Db 731 TTPPTT-----SEVSTPTTTKEPTTIHK 753

RESULT 6
US-11-169-232-74
; Sequence 74, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.

NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-11-169-232-104

Query Match 6.6%; Score 204; DB 7; Length 1140;
Best Local Similarity 41.8%; Pred. No. 1.2e-06;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LGPSTT-TPTPTT-----PTTP-----TTTTPSPPTP-----TTTTPSPPTT--TPSPT 457
DB 733 LAPTTTKEPTSTSDKPAPTTKGTAPTTPKPAPTTPKPAPTTKGTAPTTLKAPPT 792
QY 458 T-----PTTT-----PSPTTPTPTPT-----PAPTT-STPSPTTTEHTSE 492
DB 793 TPKPAPKELAPTTTGTSTSDKPAPTTKGTAPTTPKPAPTTPKPAPTT-----TPE 848
QY 493 TPKYTYVDGHLIKCYKEGDIP-----HPTNIHK 521
DB 849 TPTPTT-----SEVSTPTTTKEPTTIHK 871

RESULT 9
US-11-169-232-44
Sequence 44, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-11-169-232-44

Query Match 6.6%; Score 204; DB 7; Length 1270;
Best Local Similarity 41.8%; Pred. No. 1.4e-06;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LGPSTT-TPTPTT-----PTTP-----TTTTPSPPTP-----TTTTPSPPTT--TPSPT 457
DB 599 LAPTTTKEPTSTSDKPAPTTKGTAPTTPKPAPTTPKPAPTTKGTAPTTLKAPPT 658
QY 458 T-----PTTT-----PSPTTPTPTPT-----PAPTT-STPSPTTTEHTSE 492
DB 659 TPKPAPKELAPTTTGTSTSDKPAPTTKGTAPTTPKPAPTTPKPAPTT-----TPE 714
QY 493 TPKYTYVDGHLIKCYKEGDIP-----HPTNIHK 521
DB 715 TPTPTT-----SEVSTPTTTKEPTTIHK 737

RESULT 10
US-11-169-232-42
Sequence 42, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-11-169-232-50

Query Match 6.6%; Score 204; DB 7; Length 1314;
Best Local Similarity 41.8%; Pred. No. 1.5e-06;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LQPSSTT-TPTPTT-----PTTP-----TTTTPSPSTTP-----TTTSPSTPTPTT--TPSPT 457
DB 643 LAPTTTKEPTSTSDKPAFTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 702
QY 458 T-----PTTT-----PSTPTPTPTPT-----PAPT--STPSPTTTEHTSE 492
DB 703 TPKPAPKELAPTTTGTSTSDKPAFTTPKGTAPTTPKEPAPTTPKEPAPTTPKPAFT-----TPE 758
QY 493 TPKYTTYVDGHLIKCYKEGDIP-----HPTNIHK 521
DB 759 TPTPTT-----SEVSTPTTTKEPTTIHK 781

RESULT 13
US-11-169-232-46
Sequence 46, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Geener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-11-169-232-46

Query Match 6.6%; Score 204; DB 7; Length 1320;
Best Local Similarity 41.8%; Pred. No. 1.5e-06;
Matches 64; Conservative 6; Mismatches 25; Indels 58; Gaps 12;
QY 413 LQPSSTT-TPTPTT-----PTTP-----TTTTPSPSTTP-----TTTSPSTPTPTT--TPSPT 457
DB 649 LAPTTTKEPTSTSDKPAFTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 708
QY 458 T-----PTTT-----PSTPTPTPTPT-----PAPT--STPSPTTTEHTSE 492
DB 709 TPKPAPKELAPTTTGTSTSDKPAFTTPKGTAPTTPKEPAPTTPKEPAPTTPKPAFT-----TPE 764
QY 493 TPKYTTYVDGHLIKCYKEGDIP-----HPTNIHK 521
DB 765 TPTPTT-----SEVSTPTTTKEPTTIHK 787

RESULT 14
US-11-169-232-60
Sequence 60, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Geener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts

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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:23:24 ; Search time 190 Seconds
(without alignments)
1283.449 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTWCQEKLTICGE 555

Sequencing table: @seq@
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : A_Geneseq 21.*
- 1: Geneseqp1980a.*
 - 2: Geneseqp1990a.*
 - 3: Geneseqp2000a.*
 - 4: Geneseqp2001a.*
 - 5: Geneseqp2002a.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004a.*
 - 9: Geneseqp2005a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	555	AAV52523	AAV52523 House dus
2	555	100.0	555	AAU96327	AAU96327 Der HWM-m
3	555	100.0	555	AAU96328	AAU96328 Der HWM-m
4	536	96.6	536	AAV52525	AAV52525 House dus
5	536	96.6	536	AAU96329	AAU96329 Der HWM-m
6	64	11.5	490	AAV52535	AAV52535 D. pteron
7	64	11.5	490	AAU96339	AAU96339 Der HWM-m
8	64	11.5	509	AAV52533	AAV52533 D. pteron
9	64	11.5	509	AAU96337	AAU96337 Der HWM-m
10	64	11.5	509	AAU96338	AAU96338 Der HWM-m

ALIGNMENTS

RESULT 1
AAV52523
ID AAV52523 standard; protein; 555 AA.

XX AAV52523;

XX 22-FEB-2000 (first entry)

XX House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.

XX Mite allergen protein; map; high molecular weight; HWM-map; allergy;
KW house dust mite; IGE; immunoglobulin E; allergen; mapB; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX Dermatophagoides farinae.

XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /note= "Signal peptide"
XX /note= "Mature PDerf98-555"

XX WO9954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX McCall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 111-113; 154pp; English.

XX This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IGE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins

XX Sequence 555 AA;

Query Match 100.0%; Score 555; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRTVCYVGTWVYHKVDPTTIEDIDPFK 60
DB 1 MKTIYAILSIMACIGLMNASIKRDNDYSKNPMRTVCYVGTWVYHKVDPTTIEDIDPFK 60
QY 61 CTHLMYGFPAKIDEXYKTIQVDPYQDDNHNSWEKRGYERFNNLRKXNPETTTISLGGM 120
DB 61 CTHLMYGFPAKIDEXYKTIQVDPYQDDNHNSWEKRGYERFNNLRKXNPETTTISLGGM 120
QY 121 EGSEKYSMDAANPTVYRQOFIQSVLDLQYKFDGLDWEYPGSLGNPKDKQNYLALV 180
DB 121 EGSEKYSMDAANPTVYRQOFIQSVLDLQYKFDGLDWEYPGSLGNPKDKQNYLALV 180

QY 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYGHNA 240
DB 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYGHNA 240
QY 241 PLYKRPDETDELHTYFNNVNTWHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDETDELHTYFNNVNTWHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPPGFISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360
DB 301 KGMSPPGFISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360
QY 361 KLAFLKELGVSGVWWSLENDDFKHCGRPKNLLKVNMMINGDERKNSFECILGPSTTTP 420
DB 361 KLAFLKELGVSGVWWSLENDDFKHCGRPKNLLKVNMMINGDERKNSFECILGPSTTTP 420
QY 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540
DB 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540
QY 481 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540
DB 481 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540
QY 541 PGTIWCQEKLTICGE 555
DB 541 PGTIWCQEKLTICGE 555

RESULT 2

AAU96327
ID AAU96327 standard; protein; 555 AA.

AC AAU96327;
XX

DT 15-JUL-2002 (first entry)
XX

DE Der HMW-map polypeptide #14.
XX

KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.

XX Dermatophagoides farinae.

OS WO200222807-A2.
XX

PN 21-MAR-2002.
XX

PD 14-SEP-2001; 2001WO-US028730.
XX

PF 14-SEP-2000; 2000US-00662293.
XX

PR (HESK-) HESKA CORP.
XX

PA Mccall CA, Hunter SW, Weber ER;
XX

PI WPI; 2002-351888/38.
XX

DR N-PSDB; ABK69571.
XX

PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 114-116; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the

CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX

SQ Sequence 555 AA;

Query Match 100.0%; Score 555; DB 5; Length 555;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIYAILISINACIGLNNASIKRDHNDYSKNPMRIVCVGTWVSVVHKVDPTIEDIDPFK 60

DB 1 MKTIYAILISINACIGLNNASIKRDHNDYSKNPMRIVCVGTWVSVVHKVDPTIEDIDPFK 60

QY 61 CTHLMYGFPAKIDVYKTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGWY 120

DB 61 CTHLMYGFPAKIDVYKTIQVDFPDYQDDNHNSEKRGYERFNNLRKNPELTMTISLGWY 120

QY 121 EGSEKYSMAANPTYRQOFIQSVLDFLQYKFDGLDLDWEYPSGRLGNPKIDKQNYLALV 180

DB 121 EGSEKYSMAANPTYRQOFIQSVLDFLQYKFDGLDLDWEYPSGRLGNPKIDKQNYLALV 180

QY 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYGHNA 240

DB 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWNNVMTYDHYHGWENFYGHNA 240

QY 241 PLYKRPDETDELHTYFNNVNTWHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300

DB 241 PLYKRPDETDELHTYFNNVNTWHYYLNNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300

QY 301 KGMSPPGFISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360

DB 301 KGMSPPGFISGEGVLSYIELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360

QY 361 KLAFLKELGVSGVWWSLENDDFKHCGRPKNLLKVNMMINGDERKNSFECILGPSTTTP 420

DB 361 KLAFLKELGVSGVWWSLENDDFKHCGRPKNLLKVNMMINGDERKNSFECILGPSTTTP 420

QY 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540

DB 421 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540

QY 481 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540

DB 481 TPSTTTTHTSETPKYTYVVDGHLIKCYKEGDI PHTNIIHKYLVCFFVNGGWWVHIMPCP 540

QY 541 PGTIWCQEKLTICGE 555

DB 541 PGTIWCQEKLTICGE 555

RESULT 3

AAU96328

ID AAU96328 standard; protein; 555 AA.

XX AAU96328;

XX 15-JUL-2002 (first entry)

XX Der HMW-map polypeptide #15.

XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.

OS Dermatophagoides farinae.

XX WO200222807-A2.

XX

1	STKRDNDSKPMRIVCVVGFWSYVHKVDYPTIEDPFKCTHLMYFAKIDEYKTYIQ	60
80	VFDPPQDDNNHNSWEKRGYERFNNLRKNPETLTWISLGGWYEGSEKYSDMAANPTTRQOF	139
61	VFDPPQDDNNHNSWEKRGYERFNNLRKNPETLTWISLGGWYEGSEKYSDMAANPTTRQOF	120
140	IQSVLDFLQEKYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYYLLTAAYS	199
121	IQSVLDFLQEKYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYYLLTAAYS	180
200	PGKKIDRAYDITKELNKLFDMMVMYTYDYHGGWENFYGHNAPLYKRDETDDELHTTFFNVN	259
181	PGKKIDRAYDITKELNKLFDMMVMYTYDYHGGWENFYGHNAPLYKRDETDDELHTTFFNVN	240
260	YTMHYYLNNGATRDKLVMGVPYPYGRAWSIEDRSKLGDPKAGKMSPPGFTISGSEGVLSYI	319
241	YTMHYYLNNGATRDKLVMGVPYPYGRAWSIEDRSKLGDPKAGKMSPPGFTISGSEGVLSYI	300
320	ELCQLFQKEBWHIQDYEYNAPYGYNDKIWVGYYDDLASISCKLAFKELGVSGVMWSLE	379
301	ELCQLFQKEBWHIQDYEYNAPYGYNDKIWVGYYDDLASISCKLAFKELGVSGVMWSLE	360
380	NDDFKGHCQPKNPLKNVHNMINGDEKNSPFCILGPSTTTPTPTTTTPTTTTPTTPTTPTT	439
361	NDDFKGHCQPKNPLKNVHNMINGDEKNSPFCILGPSTTTPTPTTTTPTTTTPTTPTTPTT	420
440	TPTTTPTSPPTTTPTTPTSPPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	499
421	TPTTTPTSPPTTTPTTPTSPPTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	480
500	VGHILIKCYKEGDI PHPTNNIHKLVCEFVNGWVWHIMPCPPGFTWCQEKLTJCIGE	555
481	VGHILIKCYKEGDI PHPTNNIHKLVCEFVNGWVWHIMPCPPGFTWCQEKLTJCIGE	536

RESULT 5
AAU96329
ID AAU96329 standard; protein: 536 AA.

XX New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
XX
PS Claim 12; Page 125-127; 16pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of

XX OS Dermatophagoides pteronyssinus.

XX FH Key Location/Qualifiers

FT Modified-site /115..117

FT Modified-site /note="Aen is N-glycosylated"

FT Modified-site 240..242

FT Modified-site /note="Aen is N-glycosylated"

XX PN WO9954349-A2.

XX PD 28-OCT-1999.

XX PF 16-APR-1999; 99WO-US008524.

XX PR 17-APR-1998; 98US-00062013.

XX PR 13-MAY-1998; 98US-0085295P.

XX PR 02-SEP-1998; 98US-0098909P.

XX PA (HESK-) HESKA CORP.

XX PI McCall CA, Hunter SW, Weber ER;

XX DR WPI; 2000-052700/04.

XX DR N-PSDB; AA238589, AA238590.

XX PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivity to mite allergens.

XX PS Claim 3; Page 147-149; 154pp; English.

XX CC This sequence represents Dermatophagoides pteronyssinus mite allergen protein (map) pDerp98-490, the mature form of pDerp98-509. pDerp98-490 has a molecular weight of 98 kD, comprising 490 amino acids, and has a high degree of homology with the D. farinae mature 98 kD allergen, mapB (AA252525). Nucleic acid molecules encoding pDerp98-490 were isolated from a D. pteronyssinus cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HWM-map) composition. CC Mite allergenic proteins and peptides, and nucleic acids encoding them, CC may be used in therapeutic compositions to modify an animal's CC hypersensitivity reaction to mite allergens. Animals that may be treated CC include mammals and birds, especially felines, canines, equines, humans, CC other pets, and work or domestic animals. The proteins or fragments may CC also be used to diagnose allergies via a skin test. The proteins and CC peptides can also be used to raise antibodies, which have a variety of CC potential uses. For example, they can be used as vaccines to passively CC immunise animals against dust mite hypersensitivity, as positive controls CC in test kits and as tools to recover desired dust mite allergens from a CC mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)

XX SQ Sequence 490 AA;

Query Match 11.5%; Score 64; DB 3; Length 490;

Best Local Similarity 100.0%; Pred. No. 2.4e-56;

Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GEEGVLSYIELCOLFQKEWHIOYDEYNNAPYNDKIWVGYYDDLASISCKLAFLEKLV 370

DB 292 GEEGVLSYIELCOLFQKEWHIOYDEYNNAPYNDKIWVGYYDDLASISCKLAFLEKLV 351

QY 371 SGVM 374

DB 352 SGVM 355

RESULT 7

AAU96339

ID AAU96339 standard; protein; 490 AA.

XX AAU96339;

XX 15-JUL-2002 (first entry)

XX

DE Der HWM-map polypeptide #26.

XX Der HWM-map; American house dust mite; anti-allergic; mite; IgE;

KW mite allergenic protein; immunoglobulin E; hypersensitivity;

KW immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX McCall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX N-PSDB; ABK69585.

XX New mite allergenic protein isolated from Dermatophagoides, designated Der HWM-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 144-146; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of CC Dermatophagoides, designated Der HWM-map protein, and its related nucleic CC acid. The Der HWM-map protein is useful for eliciting an immune response CC against Der HWM-map protein. The protein or a reagent comprising a non- CC proteinaceous epitope is useful for identifying an animal (e.g., dog, CC cat) susceptible to or having an allergic response to a mite. A CC therapeutic composition is useful for desensitising a host animal to an CC allergic response to a mite. The DNA and protein can be used in the CC detection of anti-Der HWM-map antibodies in animal fluids, and inhibition CC of immunoglobulin (Ig)E or Der HWM-map protein activity associated with a CC disease. Antibodies that bind to Der HWM-map are useful for inhibiting CC binding of proteins to IgE, to prevent immunocomplex formation, thus CC reducing hypersensitivity responses to mite allergens, and as vaccines CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 CC represent Der HWM-map polypeptides of the invention

XX SQ Sequence 490 AA;

Query Match 11.5%; Score 64; DB 5; Length 490;

Best Local Similarity 100.0%; Pred. No. 2.4e-56;

Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GEEGVLSYIELCOLFQKEWHIOYDEYNNAPYNDKIWVGYYDDLASISCKLAFLEKLV 370

DB 292 GEEGVLSYIELCOLFQKEWHIOYDEYNNAPYNDKIWVGYYDDLASISCKLAFLEKLV 351

QY 371 SGVM 374

DB 352 SGVM 355

RESULT 8

AAU96339

ID AAU96339 standard; protein; 509 AA.

XX AAU96339;

XX 06-AUG-2003 (revised)

XX 22-FEB-2000 (first entry)

XX D. pteronyssinus 98 kD mite allergen protein (map) pDerp98-509.

XX Mite allergen protein; map; high molecular weight; HWM-map; allergy;

KW house dust mite; IgE; immunoglobulin E; allergen; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

```

KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "signal peptide"
FT 20..509
FT /note= "Mature PDerp98-509"
XX
XX WO9954349-A2.
XX
XX 28-OCT-1999.
XX
XX 16-APR-1999; 99WO-US008524.
XX
XX 17-APR-1998; 98US-00062013.
XX
XX 13-MAY-1998; 98US-0085295P.
XX
XX 02-SEP-1998; 98US-0098909P.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Hunter SW, Weber ER;
XX
XX WPI; 2000-052700/04.
XX
XX N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
XX
XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX used to modify an animals' hypersensitivity to mite allergens.
XX
XX Claim 3; Page 134-136; 154pp; English.
XX
XX This sequence represents Dermatophagoides pteronyssinus mite allergen
XX protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD,
XX comprising 509 amino acids, and has a high degree of homology with the D.
XX farinae 98 kD allergen, mapB (AAV52523). Nucleic acid molecules encoding
XX PDerp98-509 were isolated from a D. pteronyssinus cDNA library by
XX hybridisation with a probe encoding the D. farinae high molecular weight
XX map (HWM-map) composition. Mite allergenic proteins and peptides, and
XX nucleic acids encoding them, may be used in therapeutic compositions to
XX modify an animal's hypersensitivity reaction to mite allergens. Animals
XX that may be treated include mammals and birds, especially felines,
XX canines, equines, humans, other pets, and work or domestic animals. The
XX proteins or fragments may also be used to diagnose allergies via a skin
XX test. The proteins and peptides can also be used to raise antibodies,
XX which have a variety of potential uses. For example, they can be used as
XX vaccines to passively immunise animals against dust mite
XX hypersensitivity, as positive controls in test kits and as tools to
XX recover desired dust mite allergens from a mixture of proteins. (Updated
XX on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 509 AA;
XX
XX Query Match 11.5%; Score 64; DB 3; Length 509;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-56;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 311 GEEGVLSTIELCQLFQKEWHIQDYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLEKLGV 370
XX |||||
XX Db 311 GEEGVLSTIELCQLFQKEWHIQDYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLEKLGV 370
XX
XX QY 371 SGVM 374
XX |||||
XX Db 371 SGVM 374
XX
XX RESULT 9
XX AAU96337
XX ID AAU96337 standard; protein; 509 AA.
XX
XX AC AAU96337;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX Der HMW-map polypeptide #24.
XX
XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX mite allergenic protein; immunoglobulin E; hypersensitivity;
XX immunocomplex formation.
XX
XX Dermatophagoides farinae.
XX
XX WO200222807-A2.
XX
XX 21-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-US028730.
XX
XX 14-SEP-2000; 2000US-00662293.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Hunter SW, Weber ER;
XX
XX WPI; 2002-351888/38.
XX
XX N-PSDB; ABK69581.
XX
XX New mite allergenic protein isolated from Dermatophagoides, designated
XX Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
XX Claim 12; Page 134-136; 161pp; English.
XX
XX The invention relates to an isolated mite allergenic protein of
XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX acid. The Der HMW-map protein is useful for eliciting an immune response
XX against Der HMW-map protein. The protein or a reagent comprising a non-
XX proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX cat) susceptible to or having an allergic response to a mite. A
XX therapeutic composition is useful for desensitising a host animal to an
XX allergic response to a mite. The DNA and protein can be used in the
XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a
XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX binding of proteins to IgE, to prevent immunocomplex formation, thus
XX reducing hypersensitivity responses to mite allergens, and as vaccines
XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX represent Der HMW-map polypeptides of the invention
XX
XX Sequence 509 AA;
XX
XX Query Match 11.5%; Score 64; DB 5; Length 509;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-56;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 311 GEEGVLSTIELCQLFQKEWHIQDYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLEKLGV 370
XX |||||
XX Db 311 GEEGVLSTIELCQLFQKEWHIQDYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLEKLGV 370
XX
XX QY 371 SGVM 374
XX |||||
XX Db 371 SGVM 374
XX
XX RESULT 10
XX AAU96338
XX ID AAU96338 standard; protein; 509 AA.
XX
XX AC AAU96338;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX Der HMW-map polypeptide #25.
XX
XX Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX mite allergenic protein; immunoglobulin E; hypersensitivity;
XX immunocomplex formation.
XX
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XX OS Dermatophagoides farinae.
XX PN WO200222807-A2.
XX PD 21-MAR-2002.
XX PF 14-SEP-2001; 2001WO-US028730.
XX PR 14-SEP-2000; 2000US-00662293.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI: 2002-351888/38.
XX DR N-PSDB; ABK69583.
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX PS Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX Claim 12; Page 139-141; 161pp; English.
XX CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX SQ Sequence 509 AA;
Query Match 11.5%; Score 64; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.5e-56;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 311 GREGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDLASISCKLAFKELGV 370
Db |||||
311 GREGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDLASISCKLAFKELGV 370
QY 371 SGVM 374
Db ||||
371 SGVM 374
Search completed: March 31, 2006, 15:26:54
Job time : 190 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:27:15 ; Search time 43 Seconds
(without alignments)
1241.868 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSLINACIGLWNAS.....IMPCPPGTWCQEKLTICGE 555

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 3

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: March 31, 2006, 15:31:45
Job time : 43 secs

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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Group 15 allergen protein short isoform.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptriformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15 0102-An isoform of the gene for Der p15 encoding a chitinase
RL allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ078741; AAY84565.1; -; mRNA.
SQ SEQUENCE 532 AA; 60953 MW; A92BFB6C3C6498ED CRC64;

Query Match 11.5%; Score 64; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 6.8e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 311 GEEGVLSYIELCOLFQKEEMHIQYDEYYNAPYGYNDKIWVGDDIASISCKLAFLELGV 370
Db 311 GEEGVLSYIELCOLFQKEEMHIQYDEYYNAPYGYNDKIWVGDDIASISCKLAFLELGV 370

Qy 371 SGVM 374
Db 371 SGVM 374

RESULT 3
Q4JK70.DERPT
ID Q4JK70.DERPT PRELIMINARY; PRT; 558 AA.
AC Q4JK70;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Group 15 allergen protein.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptriformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15-A chitinase allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ078740; AAY84564.1; -; mRNA.
SQ SEQUENCE 558 AA; 63497 MW; 3CBFD8C829D4CEB8 CRC64;

Query Match 11.5%; Score 64; DB 2; Length 558;
Best Local Similarity 100.0%; Pred. No. 7.1e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 311 GEEGVLSYIELCOLFQKEEMHIQYDEYYNAPYGYNDKIWVGDDIASISCKLAFLELGV 370
Db 311 GEEGVLSYIELCOLFQKEEMHIQYDEYYNAPYGYNDKIWVGDDIASISCKLAFLELGV 370

Qy 371 SGVM 374
Db 371 SGVM 374

Search completed: March 31, 2006, 15:30:57
Job time : 237 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:31:15 ; Search time 47 Seconds
(without alignments)
976.277 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLNNAS.....IMCPPGTTWCQKLTICGE 555

Sequences: 60.0, Gapext 60.0
Gapop 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 35
Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
 - 2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
 - 3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
 - 4: /cgn2_6/ptodata/1/iaa/PCUS COMB.pcp.*
 - 5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	555	100.0	555	2	US-09-292-225-15	Sequence 15, Appl
2	555	100.0	555	2	US-09-292-225-18	Sequence 18, Appl
3	536	96.6	536	2	US-09-292-225-21	Sequence 21, Appl
4	64	11.5	490	2	US-09-292-225-41	Sequence 41, Appl
5	64	11.5	509	2	US-09-292-225-35	Sequence 35, Appl
6	64	11.5	509	2	US-09-292-225-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295

; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match 100.0%; Score 555; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTIYAILSIMACIGLNNASIKRDNDYSKNPMRIVCVGTWTSVYHKVDPVTIEDIDPFK 60
Db 1 MKTIYAILSIMACIGLNNASIKRDNDYSKNPMRIVCVGTWTSVYHKVDPVTIEDIDPFK 60
Qy 61 CTHLMYGFADIDYKTIQVDFPDYODDNNHNSWEKRGYERFNRLKNPDLTMTISLGWY 120
Db 61 CTHLMYGFADIDYKTIQVDFPDYODDNNHNSWEKRGYERFNRLKNPDLTMTISLGWY 120
Qy 121 EGSEKYSDMAANPTTQFIOQVLDLQYKFDGLDWEYPSGRLGNPKIDKQNYLALV 180
Db 121 EGSEKYSDMAANPTTQFIOQVLDLQYKFDGLDWEYPSGRLGNPKIDKQNYLALV 180
Qy 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDMMNMTYDYGWENPYGHNA 240
Db 181 RELKDAPEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDMMNMTYDYGWENPYGHNA 240
Qy 241 PLYKRPDETDLHTYFNWYTMHYLLNNGATRDKLVMGVPYGYRAWSIEDRSKLGDP 300
Db 241 PLYKRPDETDLHTYFNWYTMHYLLNNGATRDKLVMGVPYGYRAWSIEDRSKLGDP 300
Qy 301 KGMSPPGPFISGEGVLSYIELCQLFOKEWHIQYDEYVYAPYNDKIWGVYDDLASISC 360
Db 301 KGMSPPGPFISGEGVLSYIELCQLFOKEWHIQYDEYVYAPYNDKIWGVYDDLASISC 360
Qy 361 KLAFLKELGVSGVMVWSLENDDFKGCPCPKNPLKNVHNMINGDEKNSFECILGSPSTTTP 420
Db 361 KLAFLKELGVSGVMVWSLENDDFKGCPCPKNPLKNVHNMINGDEKNSFECILGSPSTTTP 420
Qy 421 TPSTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Db 421 TPSTTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
Qy 481 TPSPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGGWWHIMPCP 540
Db 481 TPSPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFVNGGWWHIMPCP 540
Qy 541 PGTWCQKLTICGE 555
Db 541 PGTWCQKLTICGE 555

RESULT 2
US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02

; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-18

Query Match 100.0%; Score 555; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTIYAALISIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFK 60
DB 1 MKTIYAALISIMACIGLMNASIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFK 60
QY 61 CTHLMYGFAKIDEXYKTYTQVDPYQDDNHNSEKGYERFNNLRKLNPELTTMISLGGWY 120
DB 61 CTHLMYGFAKIDEXYKTYTQVDPYQDDNHNSEKGYERFNNLRKLNPELTTMISLGGWY 120
QY 121 EGSEKYSDMAANTYRQFIQSVLDFLQYKFDGLDWEYPGSRLGNPKIDKQNYLALV 180
DB 121 EGSEKYSDMAANTYRQFIQSVLDFLQYKFDGLDWEYPGSRLGNPKIDKQNYLALV 180
QY 181 RELKDAFEPHGYLLTAASVPGKIDRAYDIKELNKLFDNMNVTYDHGGWENFYGNA 240
DB 181 RELKDAFEPHGYLLTAASVPGKIDRAYDIKELNKLFDNMNVTYDHGGWENFYGNA 240
QY 241 PLYKRPDELTHTYFNVTYWHYYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300
DB 241 PLYKRPDELTHTYFNVTYWHYYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPGA 300
QY 301 KGMSPPGFISGBEGVLSYIELQFLQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360
DB 301 KGMSPPGFISGBEGVLSYIELQFLQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISC 360
QY 361 KLAFLKELGVSGVMWSLENDDPKHCGPKNPLLNKVNMMINGDEKNSFECILGSPSTTP 420
DB 361 KLAFLKELGVSGVMWSLENDDPKHCGPKNPLLNKVNMMINGDEKNSFECILGSPSTTP 420
QY 421 TPTTTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
DB 421 TPTTTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 481 TSPPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCP 540
DB 481 TSPPTTHTSETPKYTYVDGHLIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCP 540
QY 541 PGTIWCQEKLTICGE 555
DB 541 PGTIWCQEKLTICGE 555

RESULT 3
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909

; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21

Query Match 96.6%; Score 536; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 SIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCTHLMYGFAKIDEXYKTYI 79
DB 1 SIKRDNDYSKNPMRIVCYVGTWSVYHKVDPTYTIEDIDPFKCTHLMYGFAKIDEXYKTYI 60
QY 80 VFDPYQDDNHNSEKGYERFNNLRKLNPELTTMISLGGWYSEKYSDMAANTYRQOF 139
DB 61 VFDPYQDDNHNSEKGYERFNNLRKLNPELTTMISLGGWYSEKYSDMAANTYRQOF 120
QY 140 IQSVLDFLQYKFDGLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASV 199
DB 121 IQSVLDFLQYKFDGLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAASV 180
QY 200 PGKIDRAYDIKELNKLFDNMNVTYDHGGWENFYGNAPLYKRPDELTHTYFNVN 259
DB 181 PGKIDRAYDIKELNKLFDNMNVTYDHGGWENFYGNAPLYKRPDELTHTYFNVN 240
QY 260 YTHYYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAGKMSPPGFISGBEGVLSYI 319
DB 241 YTHYYLNNGATRDKLVMGVPPFYGRAWSIEDRSKLGDPAGKMSPPGFISGBEGVLSYI 300
QY 320 ELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGVSGVMWSLE 379
DB 301 ELCQLFQKEWHIQYDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGVSGVMWSLE 360
QY 380 NDDPKHCGPKNPLLNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT 439
DB 361 NDDPKHCGPKNPLLNKVNMMINGDEKNSFECILGSPSTTPTTPTTPTTPTTPTTPTTPT 420
QY 440 TPTTTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 499
DB 421 TPTTTPPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 480
QY 500 VDGHILIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCPPGTIWCQEKLTICGE 555
DB 481 VDGHILIKCYKEGDIHPHTNIHKYLVCFFVNGGWWHIMPCPPGTIWCQEKLTICGE 536

RESULT 4
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13

; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41

Query Match 11.5%; Score 64; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GEEGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGV 370
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Db 292 GEEGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGV 370
|||||
QY 371 SGVM 374
|||||
Db 352 SGVM 355

RESULT 5

US-09-292-225-35
; Sequence 35, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35

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Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 311 GEEGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGV 370
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QY 371 SGVM 374
|||||
Db 371 SGVM 374

RESULT 6

US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.

; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match 11.5%; Score 64; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GEEGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGV 370
|||||
Db 311 GEEGVLSYIELCQLFQKEWHIQDEYNNAPYGYNDKIWVGYYDDLASISCKLAFLKELGV 370
|||||
QY 371 SGVM 374
|||||
Db 371 SGVM 374

Search completed: March 31, 2006, 15:32:38
Job time : 48 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 15:43:20 ; Search time 24 Seconds
(without alignments)
703.969 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIMCQEKLTICGE 555

Scoring table: 60.0
Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size: 3
Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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No matches found

Search completed: March 31, 2006, 15:46:30
Job time : 24 secs

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